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From: Kaufman, Claire
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Subject: sequence 09/783,931

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX: Rem 4C70
Room: Rem 4E85 Serial #: 09/783,931 Date: 12/23/04

11/23/2004
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Please search SEQ ID NO:2, 12, 13, 23 in commercial and interference databases.

Thanks,
Claire Kaufman, AU 1646
Rem 4E85 (571) 272-0873

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Searcher: _____
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Date Searcher Picked up: _____
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Searcher Prep/Rev. Time: _____
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Type of Search
NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

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STN: _____
DIALOG: _____
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4

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OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:57 ; Search time 40 Seconds
 (without alignment)
 290.141 Million cell updates/sec

Title: US-09-783-931-23
 Perfect score: 926
 Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSYYVISEEKDECYIA 175

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cggn2_6/ptodata/1/iaa/5A_COMB.pep:
 2: /cggn2_6/ptodata/1/iaa/5B_COMB.pep:
 3: /cggn2_6/ptodata/1/iaa/6A_COMB.pep:
 4: /cggn2_6/ptodata/1/iaa/6B_COMB.pep:
 5: /cggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
 6: /cggn2_6/ptodata/1/iaa/backfile1.pep:
 * Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	916	98.9	175	3 US-08-981-392-23 Sequence 23, Appl
2	916	98.9	175	4 US-09-908-322-23 Sequence 23, Appl
3	631.5	68.2	118	3 US-08-981-392-17 Sequence 17, Appl
4	631.5	68.2	118	4 US-09-908-322-17 Sequence 17, Appl
5	527.5	57.0	702	3 US-09-068-740A-4 Sequence 4, Appl
6	527.5	57.0	723	3 US-09-068-740A-9 Sequence 9, Appl
7	527.5	57.0	723	4 US-09-423-753-27 Sequence 27, Appl
8	527.5	57.0	723	4 US-09-641-612-6 Sequence 6, Appl
9	527.5	57.0	723	4 US-10-140-002-346 Sequence 346, Appl
10	448	48.4	713	3 US-08-872-855-5 Sequence 5, Appl
11	428	46.2	720	3 US-08-872-855-4 Sequence 4, Appl
12	419	45.2	722	3 US-08-981-392-12 Sequence 12, Appl
13	419	45.2	722	4 US-09-908-322-12 Sequence 12, Appl
14	388	41.9	728	3 US-08-981-392-2 Sequence 2, Appl
15	388	41.9	728	4 US-09-908-322-2 Sequence 2, Appl
16	388	41.9	729	3 US-08-872-855-8 Sequence 8, Appl
17	359.5	38.8	187	3 US-08-981-392-46 Sequence 46, Appl
18	359.5	38.8	187	4 US-09-908-322-46 Sequence 46, Appl
19	356	38.4	721	3 US-08-872-855-7 Sequence 7, Appl
20	356	38.4	721	3 US-08-981-392-5 Sequence 5, Appl
21	356	38.4	721	4 US-09-908-322-5 Sequence 5, Appl
22	294.5	31.8	717	3 US-08-872-855-9 Sequence 9, Appl
23	197	21.3	578	3 US-08-981-392-13 Sequence 13, Appl
24	197	21.3	578	4 US-09-908-322-13 Sequence 13, Appl
25	167	18.0	173	3 US-08-981-392-18 Sequence 18, Appl
26	167	18.0	173	4 US-09-908-322-18 Sequence 18, Appl
27	127.5	13.8	685	3 US-08-872-855-2 Sequence 2, Appl

28	127.5	13.8	685	4 US-09-641-612-7 Sequence 7, Appl
29	126.5	13.7	659	4 US-09-423-753-3 Sequence 3, Appl
30	126.5	13.7	685	4 US-09-423-753-25 Sequence 25, Appl
31	126.5	13.7	685	4 US-10-140-002-88 Sequence 88, Appl
32	125	13.5	26	3 US-08-981-392-77 Sequence 77, Appl
33	125	13.5	26	4 US-09-908-322-77 Sequence 77, Appl
34	88.5	9.6	1106	4 US-09-538-092-874 Sequence 874, App
35	82	8.9	407	4 US-09-468-433C-26 Sequence 26, Appl
36	81	8.7	233	4 US-09-311-021-46 Sequence 46, Appl
37	81	8.7	330	4 US-09-252-991A-24637 Sequence 24637, A
38	80.5	8.7	950	4 US-10-009-332-21 Sequence 1, Appl
39	77	8.3	127	4 US-09-489-039A-8856 Sequence 8856, Ap
40	76.5	8.3	874	3 US-09-369-364A-15 Sequence 15, Appl
41	75	8.1	439	4 US-09-724-797-86 Sequence 86, Appl
42	75	8.1	3025	6 5223423-3 Patent No. 5223423
43	74.5	8.0	78	4 US-09-252-991A-19604 Sequence 19604, A
44	74.5	8.0	129	4 US-09-252-991A-16731 Sequence 16731, A
45	74.5	8.0	157	4 US-09-252-991A-31989 Sequence 31989, A

ALIGNMENTS

RESULT 1	US-08-981-392-23				
	; Sequence 23, Application US/08981392				
	; Patent No. 6262025				
	GENERAL INFORMATION:				
	; APPLICANT: Ish-Horowicz, David				
	; APPLICANT: Henrique, Domingos Manuel Pinto				
	; APPLICANT: Lewis, Julian Hart				
	; APPLICANT: Artavanis-Tsakonas, Spyridon				
	; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES				
	; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON				
	; NUMBER OF SEQUENCES: 94				
	; CORRESPONDENCE ADDRESS:				
	; ADDRESSEE: Pennie & Edmonds LLP				
	; STREET: 1115 Avenue of the Americas				
	; CITY: New York				
	; STATE: NY				
	; COUNTRY: USA				
	; ZIP: 10036/2711				
	COMPUTER READABLE FORM:				
	; MEDIUM TYPE: Diskette				
	; COMPUTER: IBM Compatible				
	; OPERATING SYSTEM: DOS				
	; SOFTWARE: FastSEQ Version 2.0				
	; CURRENT APPLICATION DATA:				
	; APPLICATION NUMBER: US/08/981,392				
	; FILING DATE: 22-DEC-1997				
	; CLASSIFICATION: 514				
	; ATTORNEY/AGENT INFORMATION:				
	; NAME: Antler, Adriane M.				
	; REGISTRATION NUMBER: 32,605				
	; INFORMATION FOR SEQ ID NO: 23:				
	; TELECOMMUNICATION INFORMATION:				
	; TELEPHONE: 212-790-9090				
	; TELEFAX: 212-869-8864				
	; TELEX: 66141 PENNIE				
	; STRANDEDNESS:				
	; LENGTH: 175 amino acids				
	; TYPE: amino acid				
	; TOPOLOGY: unknown				
	; MOLECULE TYPE: peptide				
	US-08-981-392-23				
	; Score 916; DB 3; Length 175;				
	; Best Local Similarity 100.0%; Pred. No. 6.3e-97;				
	; Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 1 TMNNLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60

Qy 61 LKGDDTAVRTSHSKRDTKQSPGSRRGPRHSGXACCGPGSGGTWGVSSWNHCSV 120
 Db 61 LKGDDTAVRTSHSKRDTKQSPGSRRGPRHSGXACCGPGSGGTWGVSSWNHCSV 120

Qy 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSNDNGFQKARYPSVDYNLVQD 175
 Db 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSNDNGFQKARYPSVDYNLVQD 175

RESULT 2
 US-09-908-322-23
 ; Sequence 23, Application US/09908322
 ; Patent No. 6783956

GENERAL INFORMATION:
 APPLICANT: Ish-Horowicz, David
 Henrique, Domingos Manuel Pinto
 Lewis, Julian Hart
 Artavanis-Tsakonas, Spyridon
 Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
 VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY

COUNTRY: USA
 ZIP: 10036/2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:
 SOFTWARE: FASTSEQ Version 2.0
 FILING DATE: 22-DEC-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Antler, Adriane M.
 REGISTRATION NUMBER: 32,605
 REFERENCE/DOCKET NUMBER: 7326-038

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 118 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

US-09-908-322-23

Query Match 68.2%; Score 631.5; DB 3; Length 118;
 Best Local Similarity 99.2%; Pred. No. 1.4e-64;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 57 LVQDLKGDDTAVRTSHSKRDTKQSPGSRRGPRHSGXACCGPGSGGTWGVSSWNH 116
 Db 1 LVQDLKGDDTAVRTSHSKRDTKQSPGSRRGPRHSGXACCGPGSGGTWGVSSWNH 59

GENERAL INFORMATION:
 APPLICANT: Ish-Horowicz, David
 Henrique, Domingos Manuel Pinto

RESULT 3
 US-08-981-392-17
 ; Sequence 17, Application US/08981392
 ; Patent No. 6262025

GENERAL INFORMATION:
 APPLICANT: Ish-Horowicz, David
 Henrique, Domingos Manuel Pinto
 Lewis, Julian Hart
 Artavanis-Tsakonas, Spyridon
 Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
 VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY

COUNTRY: USA
 ZIP: 10036/2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:
 SOFTWARE: FastSEQ Version 2.0
 FILING DATE: 22-DEC-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Antler, Adriane M.
 REGISTRATION NUMBER: 32,605
 REFERENCE/DOCKET NUMBER: 7326-038

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 118 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

US-08-981-392-17

Query Match 68.2%; Score 631.5; DB 3; Length 118;
 Best Local Similarity 99.2%; Pred. No. 1.4e-64;
 Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 117 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSNDNGFQKARYPSVDYNLVQD 175
 Db 60 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSNDNGFQKARYPSVDYNLVQD 118

GENERAL INFORMATION:
 APPLICANT: Ish-Horowicz, David
 Henrique, Domingos Manuel Pinto

RESULT 4
 US-09-908-322-17
 ; Sequence 17, Application US/09908322
 ; Patent No. 6783956

GENERAL INFORMATION:
 APPLICANT: Ish-Horowicz, David
 Henrique, Domingos Manuel Pinto

Query Match 98.9%; Score 916; DB 4; Length 175;
 Best Local Similarity 100.0%; Pred. No. 6.3e-97;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 1 TMNNLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60

Qy 61 LKGDDTAVRTSHSKRDTKQSPGSRRGPRHSGXACCGPGSGGTWGVSSWNHCSV 120
 Db 61 LKGDDTAVRTSHSKRDTKQSPGSRRGPRHSGXACCGPGSGGTWGVSSWNHCSV 120

Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF Vertebrate Delta Gene and Methods Based Thereon

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-908-322-17

Query Match 68.2%; Score 631.5; DB 4; Length 118;
Best Local Similarity 99.2%; Pred. No. 1.4e-64;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps - 1;

Qy 57 LVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRGPRPHSGXACCGPGSGGCTWGSSW-H 59
Db 1 LVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRGPRPHSGXACCGPGSGGCTWGSSW-H 59

Qy 117 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSYYVISEEKDECYIA 175
Db 60 CSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSYYVISEEKDECYIA 118

RESULT 5
US-09-068-740A-4
Sequence 4, Application US/09068740A
Patent No. 6337387
GENERAL INFORMATION:
APPLICANT: SAKANO, SEIJI
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09-068-740A-4
PRIORITY NUMBER: 08/981,392
CURRENT FILING DATE: 1996-11-15
PRIORITY FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1

NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 702
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-740A-4

Query Match 57.0%; Score 527.5; DB 3; Length 702;
Best Local Similarity 64.8%; Pred. No. 1.2e-51;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNLLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 568 TMNLLANCOREKDISVSIIGATQKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 625

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRG-PRPHSGXACCGPGSGGCTWGSSW-NHCSV 119
Db 626 LKGDDTAVRDAHSKRDTCQPGSSGEEKGTTPLRG-- 662

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSYYVISEEKDECYIA 175
Db 663 --- --GEASERKRPDSGCSTS KDTKYQSYYVISEEKDECYIA 699

RESULT 6
US-09-068-740A-9
Sequence 9, Application US/09068740A
Patent No. 6337387
GENERAL INFORMATION:
APPLICANT: SAKANO, SEIJI
FILE REFERENCE: ITOH, AKIRA
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE NUMBER: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: JP 7-299611
PRIOR FILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: JP 7-311811
PRIOR FILING DATE: 1995-11-30
PRIOR APPLICATION NUMBER: PCT/JP96/03356
PRIOR FILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 9
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
US-09-068-740A-9

Query Match 57.0%; Score 527.5; DB 3; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.3e-51;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNLLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNLLANCOREKDISVSIIGATQKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRG-PRPHSGXACCGPGSGGCTWGSSW-NHCSV 119
Db 647 LKGDDTAVRDAHSKRDTCQPGSSGEEKGTTPLRG-- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSYYVISEEKDECYIA 175
Db 684 --- --GEASERKRPDSGCSTS KDTKYQSYYVISEEKDECYIA 720

RESULT 7
US-09-423-753-27
Sequence 27, Application US/09423753
Patent No. 6664098
GENERAL INFORMATION:
APPLICANT: SAKANO, SEIJI

RESULT 8
US-09-641-612-6
; TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR
; FILE REFERENCE: KP-8693
; CURRENT APPLICATION NUMBER: US/09/423,753
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/JP98/02104
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 9/124064
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-423-753-27

Query Match 57.0%; Score 527.5; DB 4; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.3e-51;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCQREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKQCSPGSRRRG-PRPHSGXACCGPGSGGGTWGVSSWNHCSV 119
Db 647 LKGDDTAVRDAHSKRDTKCQPQGSSGEEKGTPPTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTRKYOSVYVISEEKDECVIA 175
Db 684 -----GEASERKRPDSGCSTSKDTRKYOSVYVISEEKDECVIA 720

RESULT 8
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-641-612-6

Query Match 57.0%; Score 527.5; DB 4; Length 723;
Best Local Similarity 64.8%; Pred. No. 1.3e-51;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCQREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKQCSPGSRRRG-PRPHSGXACCGPGSGGGTWGVSSWNHCSV 119
Db 647 LKGDDTAVRDAHSKRDTKCQPQGSSGEEKGTPPTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTRKYOSVYVISEEKDECVIA 175
Db 684 -----GEASERKRPDSGCSTSKDTRKYOSVYVISEEKDECVIA 720

RESULT 10
US-08-872-855-5
; Sequence 5, Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,855
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 514

RESULT 9
US-10-140-002-346
; Sequence 346, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:

ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35, 430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-872-855-5

Query Match 48.4%; Score 448; DB 3; Length 713;
Best Local Similarity 54.3%; Pred. No. 1.6e-42;
Matches 95; Conservative 13; Mismatches 23; Indels 44; Gaps 3;

Qy 1 TMNLLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 580 TMNLLANCOREKDVSVSIIGATQIKNTNKADF-KARYPTVDYNLIRD 637

Qy 61 LKGDDDTAVRTSHSKRDTKQCSPGSGRRRGPRPHSGXACCGPGSSGGTWGVSSWNHCSV 120
Db 638 LKGDEATVRDAHSKRDTKCSQSGSAGEEKSTSLRG----- 673

Qy 121 LPKCSHAFIVDFLYFPFSEASERKRPDSCSTSNDTQYQSVVVISEEKDECVIA 175
Db 674 -----GEVDRKRPESYSTSNDTQYQSVVVLSAEKDECVIA 710

RESULT 11 US-08-872-855-4
Patent No. 6121045

GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872, 855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35, 430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-981-392-12

ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35, 430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-872-855-4

Query Match 46.2%; Score 428; DB 3; Length 720;
Best Local Similarity 53.7%; Pred. No. 3.1e-40;
Matches 94; Conservative 12; Mismatches 25; Indels 44; Gaps 4;

Qy 1 TMNLLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 587 TMNLLANCOREKDVSVSIIGATQIKNTNKADF-HGDHGAEKSSF-KVRYPTVDYNLIRD 644

Qy 61 LKGDDDTAVRTSHSKRDTKQCSPGSGRRRGPRPHSGXACCGPGSSGGTWGVSSWNHCSV 120
Db 645 LKGDEATVRDTHSKRDTKCSQSSAGEEK-----IAPTLRG----- 680

Qy 121 LPKCSHAFIVDFLYFPFSEASERKRPDSCSTSNDTQYQSVVVISEEKDECVIA 175
Db 681 -----GEVDRKRPESYSTSNDTQYQSVVVLSAEKDECVIA 717

RESULT 12 US-08-981-392-12
Sequence 12, Application US/08981392
Patent No. 6262025

GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Enrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981, 392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32, 605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-08-981-392-12

Query Match 45.2%; Score 419; DB 3; Length 722;
Best Local Similarity 52.6%; Pred. No. 3.3e-39;
Matches 92; Conservative 12; Mismatches 27; Indels 44; Gaps 4;

Qy 1 TMNLLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 589 TMNLLANCOREKDVSVSIIGATQIKNTNKADF-HGDHGAEKSSF-KVRYPTVDYNLIRD 646

Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF Vertebrate Delta Gene and Methods Based Thereon

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,322

FILING DATE: 17-JUL-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S Leslie
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 728 amino acid
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

us-09-908-322-2

Query Match 41.9%; Score 388; DB 4; Length 728;
Best Local Similarity 49.7%; Pred. No. 1.2e-35;
Matches 87; Conservative 15; Mismatches 27; Indels 46; Gaps 5;

Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKRADFXGDXSSDKNGFOKARYPSVDYNLVQD 60
Db 597 TMNNLANCOREKDISISVIGATIQLNTNKKVDFH--SDNSDKNGY-KVRYPSVDYNLVHE 653

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRGPRPHSGXACCGPGSGGGTWGVSSWNHCSV 120
Db 654 LKNED-SVKEEHGKEAKCETYDSEAEERKS----- -AVQ 685

Qy 121 LPKCSHAFIGVDFLYPPSGEASERKRPDSGCSTSNDTKYQSVVVISEEKDECYIA 175
Db 686 LK-----SSDTSERKRPDSVYSTSDTKYQSVVVISEEKDECYIA 725

Search completed: December 2, 2004, 04:03:16
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:12 ; Search time 194 Seconds
 (without alignments)
 519.024 Million cell updates/sec

Title: US-09-783-931-23
 Perfect score: 926
 Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSYYVISEEKDECYIA 175

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	527.5	57.0	723	1	DLL1_HUMAN	000548	homo sapien
2	445	48.1	714	1	DLL1_RAT	P97677	rattus norvegicus
3	431	46.5	722	2	Q6PFV7	Q6pfv7	mus musculus
4	431	46.5	722	2	AAH57400	Aah57400	mus musculus
5	431	46.5	722	2	AAR30869	Aar30869	mus musculus
6	431	46.5	722	2	AAH65063	Aah65063	mus musculus
7	428	46.2	722	1	DLL1_MOUSE	O61483	mus musculus
8	388	41.9	728	2	Q90656	Q90656	gallus gallus
9	387.5	41.8	726	2	Q8AW87	Q8aw87	cynops pyrrhura
10	356	38.4	721	2	Q91902	Q91902	xenopus laevis
11	294.5	31.8	717	2	P87357	P87357	brachydanio
12	294.5	31.8	720	2	Q8UWJ4	Q8uwj4	brachydanio
13	218	23.5	772	2	Q6DI48	Q6di48	brachydanio
14	149	16.1	802	2	Q57462	Q57462	brachydanio
15	126.5	13.7	685	1	DLL4_HUMAN	Q9nr61	homo sapien
16	126.5	13.7	686	1	DLL4_MOUSE	Q9j171	mus musculus
17	125.5	13.6	686	2	Q9DBU9	Q9dbu9	mus musculus
18	91	9.8	364	2	Q6MZM8	Q6mzm8	homo sapien
19	91	9.8	364	2	Q6N000	Q6n000	homo sapien
20	91	9.8	364	2	CAE45875	Cae45875	homo sapien
21	91	9.8	364	2	CAE45984	Cae45984	homo sapien
22	91	9.8	364	2	CAE46001	Cae46001	homo sapien
23	88.5	9.6	1106	1	GLI1_HUMAN	P08151	homo sapien
24	87.5	9.4	906	2	Q817K4	Q8i7k4	caenorhabditis elegans
25	87.5	9.4	1837	2	Q95ZU1	Q95zui	caenorhabditis elegans
26	87.5	9.4	1839	2	Q17383	Q17383	caenorhabditis elegans
27	86.5	9.3	167	2	Q8CEA2	Q8cea2	mus musculus
28	86.5	9.3	945	2	Q6XGW8	Q6xgw8	hepatitis b virus
29	86.5	9.3	845	2	AAP79719	Aap79719	drosophila melanogaster
30	86.5	9.3	1561	1	Y34F_DROME	Y34f_drome	drosophila melanogaster
31	84.5	9.1	845	2	Q6XGM0	Q6xgm0	hepatitis b virus

ALIGNMENTS

32	84.5	9.1	845	2	Q6XGR9	Q6xgr9	hepatitis b virus
33	84.5	9.1	845	2	AAP79768	Aap79768	hepatitis b virus
34	84.5	9.1	845	2	AAP79817	Aap79817	hepatitis b virus
35	84	9.1	407	1	MGB6_HUMAN	Q86uz3	homo sapien
36	84	9.1	541	2	Q86UZ3	Q86uz3	homo sapien
37	83.5	9.0	1651	1	ROB1_RAT	Q6zde6	rattus norvegicus
38	83	9.0	438	2	Q6ZDE6	Q6zde6	oryza sativa
39	83	9.0	438	2	BAD09364	Bad09364	oryza sativa
40	83	9.0	657	2	Q8JXJ8	Q8jxj8	oryza sativa
41	83	9.0	1694	2	Q17652	Q17652	caenorhabditis elegans
42	82.5	8.9	845	2	Q6XGR2	Q6xgr2	hepatitis b virus
43	82.5	8.9	1431	1	CA1G_MESAU	Q9jmh4	mesocricetus auratus
44	82.5	8.9	311	2	Q8H077	Q8h077	oryza sativa

RESULT 1
 DLL1_HUMAN STANDARD;
 ID DLL1_HUMAN STANDARD;
 AC 000548; Q9NU41; Q9UJV2;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)
 DE (H-Delta-1) (UNQ146/PRO172).
 GN Name= DLL1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TAXID=9606;

[1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99180765; PubMed=10079256;
 RX Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowicz D., Artavanis-Tsakonas S.; "Human ligands of the Notch receptor." Am. J. Pathol. 154:785-794 (1999).
 RA [2]
 RN SEQUENCE FROM N.A.
 RP Han W., Ye Q., Moore M.A.S.; "A soluble form of human delta-like-1 inhibits differentiation of hematopoietic progenitor cells." Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RP Oda T., Chandrasekharappa S.C.; "Human Delta 1 gene sequence." Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A.
 RP Han W., Ye Q., Moore M.A.S.; "A soluble form of human delta-like-1 inhibits differentiation of hematopoietic progenitor cells." Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RL [5]
 RN SEQUENCE FROM N.A.
 RP Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang Z., Godowski P.; "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment." Genome Res. 13:2265-2270 (2003).
 RL [5]
 RN SEQUENCE FROM N.A.
 RP Almeida J.; "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment." Genome Res. 13:2265-2270 (2003).
 RL [6]
 RN FUNCTION.

RX MEDLINE=21464863; PubMed=11581320;
 RA Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,
 RA Henrique D., Parreira L.;
 RT "Differential effects of Notch ligands Delta-1 and Jagged-1 in human
 RT lymphoid differentiation.";
 RL J. Exp. Med. 194:991-1001 (2001).
 CC -1- FUNCTION: Acts as a ligand for Notch receptors. Blocks the
 CC differentiation of progenitor cells into the B-cell lineage while
 CC promoting the emergence of a population of cells with the
 CC characteristics of a T-cell/NK-cell precursor.
 CC -1- SUBUNIT: Interacts with Notch receptors.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower
 CC expression in brain and muscle and almost no expression in
 CC placenta, lung, liver, and kidney.
 CC -1- SIMILARITY: Contains 1 DSL domain.
 CC -1- SIMILARITY: Contains 8 EGF-like domains.

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DR AF003522; AAB61286.1; -.
 DR EMBL; AF196571; AAF05834.1; -.
 DR EMBL; AF222310; AAG09716.1; -.
 DR EMBL; AY358892; AAQ89251.1; -.
 DR EMBL; AL078605; CAB89569.1; -.
 DR HSSP; P00740; 1EDM.
 DR Genew; HGNC:2908; DLL1.
 DR MIM; 606582; -.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005112; F:Notch binding; IPI.
 DR GO; GO:00030154; P:cell differentiation; TAS.
 DR GO; GO:0001709; P:cell fate determination; TAS.
 DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
 DR GO; GO:0009912; P:hair cell fate commitment; ISS.
 DR GO; GO:0030097; P:hemopoiesis; NAS.
 DR GO; GO:0042472; P:inner ear morphogenesis; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR GO; GO:0007219; P:Notch signaling pathway; NAS.
 DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
 DR GO; GO:0030155; P:regulation of cell adhesion; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR001774; DSL.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_Like.
 DR Pfam; PF01414; DSL; 1.
 DR Pfam; PF00008; EGF; 6.
 DR PRINTS; PR00010; EGFBLOOD.
 DR SMART; SM00051; DSL; 1.
 DR SMART; SM000179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 8.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS50026; EGF_3; 7.
 DR PROSITE; PS01187; EGF_CA; 1.
 KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
 KW Repeat; Signal; Transmembrane.

FT SIGNAL 1 17 Potential:
 FT CHAIN 18 723 Delta-like protein 1.
 FT DOMAIN 18 545 Extracellular (Potential).
 FT TRANSMEM 546 568 Potential.
 FT DOMAIN 569 723 Cytoplasmic (Potential).
 FT DOMAIN 159 221 DSL.
 FT DOMAIN 226 254 EGF-like 1.
 FT DOMAIN 257 285 EGF-like 2.

Query Match 57.0%; Score 527.5; DB 1; Length 723;
 Best Local Similarity 64.8%; Pred. No. 2.7e-43;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFOKARYPSVSDYNLVQD 60
 Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

QY 61 LKGDDTAVRTSHSKRDTKQSPGSQRGG-PRPHSGXACCGPGSGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQPGSSGEEKGTPTTLRG----- 683

QY 120 SLPKCSHAFIVDFLYPPSGEASERKRPDSCSTSKDTRXQSYYVISEEKDECYIA 175
 Db 684 -----GEASERKRPDSCSTSKDTRXQSYYVISEEKDECYIA 720

RESULT 2
 DLL1_RAT
 ID DLL1_RAT STANDARD; PRT; 714 AA.
 AC P97677;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1).
 GN Name=Dll1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Disibio G., Hebshi L., Boultier J., Weinmaster G.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: May be involved in cell-to-cell communication in
 CC mammalian embryos. May have a role in cellular interactions
 CC underlying somitogenesis and development of the nervous system (By
 similarity).

CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.	FT	DISULFID	374	390	By similarity.
CC	-!- SIMILARITY: Contains 1 DSL domain.	FT	DISULFID	392	401	By similarity.
CC	-!- SIMILARITY: Contains 8 EGF-like domains.	FT	DISULFID	408	419	By similarity.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	FT	DISULFID	413	428	By similarity.
CC	EMBL: U78889; AAB37343.11; - .	FT	DISULFID	430	439	By similarity.
DR	HSSP; P08709; 1BF9.	FT	DISULFID	446	466	By similarity.
DR	RGD; 70949; D111.	FT	DISULFID	468	477	By similarity.
DR	GO; GO:0005576; C:extracellular; ISS. C:integral to plasma membrane; ISS.	FT	DISULFID	484	495	By similarity.
DR	GO; GO:0005887; F:Notch binding; IPI.	FT	DISULFID	489	504	By similarity.
DR	GO; GO:0030154; P:cell differentiation; ISS.	FT	DISULFID	506	515	By similarity.
DR	GO; GO:0001709; P:cell fate determination; ISS.	FT	CARBOHYD	476	476	N-linked (GlcNAc. . .) (Potential).
DR	GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.	SEQUENCE	714 AA;	77378 MW;	4B8EE2272BAEA27E CRC64;	
DR	GO; GO:009912; P:hair cell fate commitment; NAS.	Query Match	48.1%;	Score 445;	DB 1;	Length 714;
DR	GO; GO:0030097; P:hemopoiesis; ISS.	Best Local Similarity	54.3%;	Pred. No. 3.7e-35;		
DR	GO; GO:0042472; P:inner ear morphogenesis; ISS.	Matches	95;	Conservative	12;	Mismatches 24;
DR	GO; GO:0007399; P:neurogenesis; NAS.	Indels	44;	Gaps	3;	
DR	GO; GO:0007219; P:Notch signaling pathway; NAS.	Qy	1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60			
DR	PRINTS: PR000010; EGFBLOOD.	Db	581 TMNNLANCQREKDVSVSIIGATQIRNTNKKADF-HGDHGADKSSF-KARYPTVDYNLIRD 638			
DR	SMART: SMART00051; DSL; 1.	Qy	61 LKGDDTAVRTSHSKRDTTKCOSPGSGRRRGPRPHSGXACCGPGSGGGTWGVSSWNHCSV 120			
DR	PROSITE; PS000010; ASX_HYDROXYL; 3.	Db	639 LKGDEATVRDAHSKRDTTKCQSQSGVGEEKSTLRG--			
DR	PROSITE; PS000022; EGF_1; 8.	Qy	121 LPKCSHAFIVDFLYFPFSGEASERKRDPDSGCSTSKDTKYQSVVVISEEKDECVIA 175			
DR	PROSITE; PS000026; EGF_2; 7.	Db	675 ---GEVPDRKRPESVYSTSKDTKYQSVVLSAEKDECVIA 711			
DR	Developmental protein; Differentiation; EGF-like domain; Glycoprotein; Repeat; Signal; Transmembrane.	RESULT 3				
DR	InterPro; IPR0000742; EGF_2.	Q6PFV7				
DR	InterPro; IPR001881; EGF_Ca.	ID	Q6PFV7	PRELIMINARY;	PRT;	722 AA.
DR	InterPro; IPR001438; EGF_II.	AC	Q6PFV7			
DR	InterPro; IPR006209; EGF_like.	DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DR	Pfam; PF01414; DSL; 1.	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DR	Pfam; PF00008; EGF; 6.	DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DR	PRINTS: PR000010; EGFBLOOD.	DB	Delta-like 1.			
DR	SMART: SMART00051; DSL; 1.	GN	Name=Dll1;			
DR	PROSITE; PS000010; ASX_HYDROXYL; 3.	OS	Mus musculus (Mouse).			
DR	PROSITE; PS000022; EGF_1; 8.	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DR	PROSITE; PS001186; EGF_2; 8.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
DR	PROSITE; PS500026; EGF_3; 7.	NCBI_TaxID=10090;	[1]			
DR	PROSITE; PS001187; EGF_CA; 2.	RN				
KW	Developmental protein; Differentiation; EGF-like domain; Glycoprotein; Repeat; Signal; Transmembrane.	RP	SEQUENCE FROM N.A.			
FT	SIGNAL	RC	STRAIN=C57BL/6; TISSUE=Mouse;			
FT	CHAIN	RX	MEDLINE=22388257; PubMed=12477932;			
FT	DOMAIN	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,' Schuler G.D., Klausner R.D., Collins F.S.,' Wagner L., Shenmen C.M.,' Schaefer C.F.,' Bhat N.K., Altschul S.F.,' Zeaberg B.,' Buetow K.H.,' Hopkins R.F.,' Jordan H.,' Moore T.,' Max S.I.,' Wang J.,' Hsieh F.,' Diatchenko L.,' Marszina K.,' Farmer A.A.,' Rubin G.M.,' Hong L., Stapleton M.,' Soares M.B.,' Bonaldo M.F.,' Casavant T.L.,' Brownstein M.J.,' Usdin T.B.,' Toshiyuki S.,' Carninci P.,' Prange C.,' Raha S.S.,' Loquellano N.A.,' Peters G.J.,' Abramson R.D.,' Mullahy S.J.,' Bosak S.A.,' McEwan P.J.,' McKernan K.J.,' Malek J.A.,' Gunaratne P.H.,' Richards S.,' Worley K.C.,' Hale S.,' Garcia A.M.,' Gay L.J.,' Blakesley R.W.,' Touchman J.W.,' Green E.D.,' Dickson M.C.,' Rodriguez A.C.,' Grimwood J.,' Schmutz J.,' Myers R.M.,' Butterfield Y.S.,' Krzywinski M.I.,' Skalska U.,' Smailus D.E.,' Schein J.E.,' Jones S.J.,' Marra M.A.,' "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";			
FT	DISULFID	RA	Villalon D.K., Muñoz D.M., Sodergren B.J., Lu X.,' Gibbs R.A.,' Fahey J.,' Helton E.,' Ketteman M.,' Madan A.,' Rodrigues S.,' Sanchez A.,' Whiting M.,' Madan A.,' Young A.C.,' Shevchenko Y.,' Bouffard G.G.,' Blakesley R.W.,' Touchman J.W.,' Green E.D.,' Dickson M.C.,' Rodriguez A.C.,' Grimwood J.,' Schmutz J.,' Myers R.M.,' Butterfield Y.S.,' Krzywinski M.I.,' Skalska U.,' Smailus D.E.,' Schein J.E.,' Jones S.J.,' Marra M.A.,' "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";			
FT	DISULFID	RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	[2]		
FT	DISULFID	RN	SEQUENCE FROM N.A.			
FT	DISULFID	RC	STRAIN=C57BL/6; TISSUE=Mouse;			
FT	DISULFID	RA	Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.			
FT	DISULFID	RL				

RN	[3]	SEQUENCE FROM N.A.	OX	NCBI_TaxID=10090;
RP		STRAIN=C57BL/6; TISSUE=Mouse;	RN	[1]
RC			RP	SEQUENCE FROM N.A.
RA			RC	SEQUENCE FROM N.A.
RA			RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Shenmen C.M., Bhat N.K., Shnayderman N.A., Buetow K.H., Schaefer C.F., Bhat N.K., Buetow K.H., Moore T., Max S.I., Rubin G.M., Hong L., Hsieh F., Farmer A.A., Bonaldo M.P., Casavant T.L., Scheetz T.E., Hopkins R.F., Jordan H., Soares M.B., Stapleton M., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Altenschul S.F., Zeeberg B., Matusina K., Diatchenko L., Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL			RL	[2]
RL			RN	SEQUENCE FROM N.A.
RA			RC	SEQUENCE=C57BL/6; TISSUE=Mouse;
RA			RA	Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
CC		- SIMILARITY: Contains 8 EGFR-like domains.	RL	Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR			DR	EMBL; BC057400; AAH57400.1; -.
DR			DR	EMBL; BC065063; AAH65063.1; -.
DR			DR	EMBL; AY497019; AAR30869.1; -.
DR			DR	GO; GO:0005515; F:protein binding; IPI.
DR			DR	GO; GO:0007386; P:compartment specification; IMP.
DR			DR	GO; GO:0007368; P:compartiment specification of left/right symmetry; IMP.
DR			DR	GO; GO:0001757; P: somite specification; IMP.
DR			DR	InterPro; IPR000152; Asx_hydroxy1_S.
DR			DR	InterPro; IPR001774; DSL.
DR			DR	InterPro; IPR000742; EGF_2.
DR			DR	InterPro; IPR001881; EGF_Ca.
DR			DR	InterPro; IPR001438; EGF_III.
DR			DR	InterPro; IPR006209; EGF-like.
DR			DR	InterPro; IPR006210; IEGF.
DR			DR	Pfam; PF01414; DSL; 1.
DR			DR	Pfam; PF00008; EGF; 6.
DR			DR	Pfam; PF07645; EGF_Ca; 1.
DR			DR	PRINTS; PR00010; EGF_BLOOD.
DR			DR	SMART; SM00051; DSL; 1.
DR			DR	SMART; SM00181; EGF; 8.
DR			DR	SMART; SM00179; EGF CA; 6.
DR			DR	PROSITE; PS00010; ASX_HYDROXYL; 3.
DR			DR	PROSITE; PS00022; EGF_1; 8.
DR			DR	PROSITE; PS01186; EGF_2; 8.
DR			DR	PROSITE; PS50026; EGF_3; 6.
DR			DR	PROSITE; PS01187; EGF_CA; 2.
KW		EGF-like domain.	SQ	SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EBC75E CRC64;
QY			QY	1 TMNNLANCQREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
DB			DB	589 TMNNLANCQREKDVSVSIIGATQIKNTNKADF-HGDHGAEKSSF-KVRYPTVDYNLVRD 646
QY			QY	61 LKGDDTAVRTSHSKRDTKQSPGSGRRRGPRPHSGXACCGPGSGGGTWGVSSWNHCSV 120
DB			DB	647 LKGDEATVRDTHSKRDTKQCSQSSAGEEK---IAPTLRG----- 682
QY			QY	121 LPRCSHAFIVDFLYFPPEASERKRPDSGCSTS SKDTKYQSYYVISSEKDEC VIA 175
DB			DB	683 ---GEIPDRKRPESYSTS SKDTKYQSYYVLSAEKDEC VIA 719
RESULT 5			ID	AAR30869 PRELIMINARY; PRT; 722 AA.
AC			AC	AAR30869; PRELIMINARY; PRT; 722 AA.
DT			DT	02-MAR-2004 (TREMBLrel. 27, Created)
DB			DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
QY			DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DB			DB	Delta-like-1.
OS		Mus musculus (Mouse)	GN	DLL1.
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC	Mus musculus (Mouse)
OC			OX	NCBI_TaxID=10090;
OC			RN	[1] SEQUENCE FROM N.A.
RC			RC	SEQUENCE=C57BL/6J;
RA			RA	Nagaraja R., Waeltz P., Brathwaite M.E.; "Genomic Sequence Analysis in the Mouse t-complex Region.";
RA			RL	Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
RA			RN	[2] SEQUENCE FROM N.A.
RC			RC	SEQUENCE=C57BL/6J;
RA			RA	Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;

DR	InterPro; IPR00742; EGF_2.	PRELIMINARY;	PRT;	728 AA.
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR001438; EGF_II.			
DR	InterPro; IPR006209; EGF_like.			
DR	Pfam; PF01414; DSL; 1.			
DR	Pfam; PF00008; EGF; 6.			
DR	PRINTS; PRO0010; EGFBLOOD.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.			
DR	PROSITE; PS00022; EGF_1; 8.			
DR	PROSITE; PS01186; EGF_2; 8.			
DR	PROSITE; PS50026; EGF_3; 7.			
DR	PROSITE; PS01187; EGF_CA; 2.			
KW	Developmental protein; Differentiation; EGF-like domain; Glycoprotein; Repeat; Signal; Transmembrane.			
FT	SIGNAL 1 17	Potential.		
FT	CHAIN 18 722	Delta-like protein 1.		
FT	DOMAIN 18 545	Extracellular (Potential).		
FT	TRANSMEM 546 568	Potential.		
FT	DOMAIN 569 722	Cytoplasmic (Potential).		
FT	DOMAIN 158 220	DSL.		
FT	DOMAIN 225 253	EGF-like 1.		
FT	DOMAIN 256 284	EGF-like 2.		
FT	DOMAIN 291 324	EGF-like 3.		
FT	DOMAIN 331 362	EGF-like 4, calcium-binding (Potential).		
FT	DOMAIN 369 401	EGF-like 5.		
FT	DOMAIN 408 439	EGF-like 6.		
FT	DOMAIN 446 477	EGF-like 7, calcium-binding (Potential).		
FT	DOMAIN 484 515	EGF-like 8.		
FT	DISULFID 225 236	By similarity.		
FT	DISULFID 229 242	By similarity.		
FT	DISULFID 244 253	By similarity.		
FT	DISULFID 256 267	By similarity.		
FT	DISULFID 262 273	By similarity.		
FT	DISULFID 275 284	By similarity.		
FT	DISULFID 291 303	By similarity.		
FT	DISULFID 297 313	By similarity.		
FT	DISULFID 315 324	By similarity.		
FT	DISULFID 331 342	By similarity.		
FT	DISULFID 336 351	By similarity.		
FT	DISULFID 353 362	By similarity.		
FT	DISULFID 369 380	By similarity.		
FT	DISULFID 374 390	By similarity.		
FT	DISULFID 392 401	By similarity.		
FT	DISULFID 408 419	By similarity.		
FT	DISULFID 413 428	By similarity.		
FT	DISULFID 430 439	By similarity.		
FT	DISULFID 446 466	By similarity.		
FT	DISULFID 468 477	By similarity.		
FT	DISULFID 484 495	By similarity.		
FT	DISULFID 489 504	By similarity.		
FT	DISULFID 506 515	By similarity.		
FT	CARBOHYD 476 476	N-linked (GlcNAc. . .) (Potential).		
SQ	SEQUENCE 722 AA; 78448 MW;	93B2D6666D2388B7 CRC64;		
Query Match		Score 41.9%;	DB 2;	Length 728;
Best Local Similarity		49.7%;	Pred. No. 1.	6e-29;
Matches	87;	Conservative	15;	Mismatches 27;
				Indels 46; Gaps 5;
QY	1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDNLVQD 60	1 LKGDDTAVRTSHSKRDTKCQSPGSGRRRGPRPHSGGXACCGPGSGGGTWGVSSWNHCSV 120		
Db	597 TMNNLANCQREKDISISVIGATQIKNNTKVKVDFH--SDNSDKNGY-KVRYPSVDNLVHE 653	61 LKGDDTAVRTSHSKRDTKCQSPGSGRRRGPRPHSGGXACCGPGSGGGTWGVSSWNHCSV 120		
QY	597 TMNNLANCQREKDISISVIGATQIKNNTKVKVDFH--SDNSDKNGY-KVRYPSVDNLVHE 653	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
Db	686 LK-----	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
RESULT 9		654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
Q8AW87		654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
ID	Q8AW87	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
AC	Q8AW87;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DT	01-MAR-2003 (TREMBLrel. 23, Created)	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DE	Ligand Delta-1.	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
GN	Name=Delta-1;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
OS	Cynops pyrrhogaster (Japanese common newt).	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
OC	Salamandroidea; Salamandridae; Caudata; Batrachia; Cynops.	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
Q90656	PRELIMINARY;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DR	InterPro; IPR00742; EGF_2.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR001438; EGF_II.			
DR	InterPro; IPR006209; EGF_like.			
DR	Pfam; PF01414; DSL; 1.			
DR	Pfam; PF00008; EGF; 6.			
DR	PRINTS; PRO0010; EGFBLOOD.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.			
DR	PROSITE; PS00022; EGF_1; 8.			
DR	PROSITE; PS01186; EGF_2; 8.			
DR	PROSITE; PS05026; EGF_3; 6.			
DR	PROSITE; PS01187; EGF_CA; 2.			
DR	SMART; SM00051; DSL; 1.			
DR	SMART; SM00179; EGF_CA; 4.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.			
DR	PROSITE; PS00022; EGF_1; 8.			
DR	PROSITE; PS01186; EGF_2; 8.			
DR	PROSITE; PS05026; EGF_3; 6.			
DR	PROSITE; PS01187; EGF_CA; 2.			
KW	EGF-like domain.			
SQ	SEQUENCE 728 AA; 79861 MW;	93B2D6666D2388B7 CRC64;		
Query Match		Score 41.9%;	DB 2;	Length 728;
Best Local Similarity		49.7%;	Pred. No. 1.	6e-29;
Matches	87;	Conservative	15;	Mismatches 27;
				Indels 46; Gaps 5;
QY	1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDNLVQD 60	1 LKGDDTAVRTSHSKRDTKCQSPGSGRRRGPRPHSGGXACCGPGSGGGTWGVSSWNHCSV 120		
Db	597 TMNNLANCQREKDISISVIGATQIKNNTKVKVDFH--SDNSDKNGY-KVRYPSVDNLVHE 653	61 LKGDDTAVRTSHSKRDTKCQSPGSGRRRGPRPHSGGXACCGPGSGGGTWGVSSWNHCSV 120		
QY	597 TMNNLANCQREKDISISVIGATQIKNNTKVKVDFH--SDNSDKNGY-KVRYPSVDNLVHE 653	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
Db	686 LK-----	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
RESULT 8		654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
Q9AW87	PRELIMINARY;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
ID	Q8AW87	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
AC	Q8AW87;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DT	01-MAR-2003 (TREMBLrel. 23, Created)	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DE	Ligand Delta-1.	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
GN	Name=Delta-1;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
OS	Cynops pyrrhogaster (Japanese common newt).	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
OC	Salamandroidea; Salamandridae; Caudata; Batrachia; Cynops.	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
Q90656	PRELIMINARY;	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
DR	InterPro; IPR00742; EGF_2.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR001438; EGF_II.			
DR	InterPro; IPR006209; EGF_like.			
DR	Pfam; PF01414; DSL; 1.			
DR	Pfam; PF00008; EGF; 6.			
DR	PRINTS; PRO0010; EGFBLOOD.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.			
DR	PROSITE; PS00022; EGF_1; 8.			
DR	PROSITE; PS01186; EGF_2; 8.			
DR	PROSITE; PS05026; EGF_3; 6.			
DR	PROSITE; PS01187; EGF_CA; 2.			
KW	EGF-like domain.			
SQ	SEQUENCE 722 AA; 79861 MW;	93B2D6666D2388B7 CRC64;		
Query Match		Score 46.2%;	DB 1;	Length 722;
Best Local Similarity		53.7%;	Pred. No. 1.	8e-33;
Matches	94;	Conservative	12;	Mismatches 25;
				Indels 44; Gaps 4;
QY	1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDNLVQD 60	1 LKGDDTAVRTSHSKRDTKCQSPGSGRRRGPRPHSGGXACCGPGSGGGTWGVSSWNHCSV 120		
Db	589 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDNLVQD 646	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
QY	61 LKGDDTAVRTSHSKRDTKCQSPGSGRRRGPRPHSGGXACCGPGSGGGTWGVSSWNHCSV 120	654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----		
Db	647 LKGDEATVRDTHSKRDTKCQSSAGEEK-----IAPTLRG-----	682		
QY	121 LPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSNDKNGFQKARYPSVDNLVQD 60	121 LPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSNDKNGFQKARYPSVDNLVQD 175		
Db	683 -----GEIPDRKRPESVYSTSKDTKyQSvVvSAEKDECIA 725	686 LK-----		
RESULT 9		686 LK-----		
Q8AW87	PRELIMINARY;	686 LK-----		
ID	Q8AW87	686 LK-----		
AC	Q8AW87;	686 LK-----		
DT	01-MAR-2003 (TREMBLrel. 23, Created)	686 LK-----		
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	686 LK-----		
DT	01-MAR-			

NCBI_TaxID=83330;	
SEQUENCE FROM N.A.	"Primary neurogenesis in Xenopus embryos regulated by a homologue of the Drosophila neurogenic gene Delta.";
RN [1]	Nakamura K., Kikuchi Y., Sasaki K., Chiba C., Saito T.; Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RA -!- SIMILARITY: Contains 8 EGF-like domains.	CC EMBL; AB095017; BAC41350.2; - . HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.	DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005509; P:cell communication; IEA.	DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.	DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; ASX ion binding; IEA.	DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR000154; P:cell communication; IEA.	DR InterPro; IPR000154; P:cell communication; IEA.
DR InterPro; IPR000154; P:calcium ion binding; IEA.	DR InterPro; IPR000154; P:calcium ion binding; IEA.
DR InterPro; IPR000174; DSL.	DR InterPro; IPR000174; DSL.
DR InterPro; IPR000174; DSL.	DR InterPro; IPR000174; DSL.
DR InterPro; IPR000742; EGF_2.	DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR000742; EGF_Ca.	DR InterPro; IPR000742; EGF_Ca.
DR InterPro; IPR001881; EGF_Ca.	DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001881; EGF_II.	DR InterPro; IPR001881; EGF_II.
DR InterPro; IPR001438; EGF_II.	DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.	DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.	DR InterPro; IPR006210; IEGF.
Pfam; PF01414; DSL; 1.	Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.	DR Pfam; PF00008; EGF; 6.
DR PRINTS; PRO0010; EGFBLOOD.	DR PRINTS; PRO0010; EGFBLOOD.
DR SMART; SM00051; DSL; 1.	DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGFC_A; 4.	DR SMART; SM00179; EGFC_A; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.	DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00010; EGFBLOOD.	DR PROSITE; PS00010; EGFBLOOD.
DR SMART; SM00051; DSL; 1.	DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.	DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_Ca; 6.	DR SMART; SM00179; EGF_Ca; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.	DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.	DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.	DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.	DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 2.	DR PROSITE; PS01187; EGF_Ca; 2.
KW EGF-like domain.	KW EGF-like domain.
SQ SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;	SQ SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;
Query Match 38.4%; Score 356; DB 2; Length 721;	Query Match 38.4%; Score 356; DB 2; Length 721;
Best Local Similarity 46.3%; Pred. NO. 2.3e-26;	Best Local Similarity 46.3%; Pred. NO. 2.3e-26;
Matches 81; Conservative 15; Mismatches 33; Indels 46; Gaps 4;	Matches 81; Conservative 15; Mismatches 33; Indels 46; Gaps 4;
1 TMNNLANCOREKDIDSVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVVDYNLVQD 60	1 TMNNLANCOREKDIDSVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVVDYNLVQD 60
590 TMNNLANCOREKDIDSVSFIGTQIKNTNKKIDF-LSESNNEKNGY-KPRYPSPVVDYNLVHE 647	590 TMNNLANCOREKDIDSVSFIGTQIKNTNKKIDF-LSESNNEKNGY-KPRYPSPVVDYNLVHE 647
61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRGPRPHSGXACCGPGSSGGGTWGVSNNHCSV 120	61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRGPRPHSGXACCGPGSSGGGTWGVSNNHCSV 120
648 LKNEDSP-KEERSKCEAKCSSNNDSDSE-----	648 LKNEDSP-KEERSKCEAKCSSNNDSDSE-----
6121 LPKCSHAFIVDFFLYFPFSGEASERKRPDSGCSTS SKDTKRYOSVVVISEEKDECVIA 175	6121 LPKCSHAFIVDFFLYFPFSGEASERKRPDSGCSTS SKDTKRYOSVVVISEEKDECVIA 175
652 LKHED-SVKEEEHGKRESKCIANGSEADEKHP-----	652 LKHED-SVKEEEHGKRESKCIANGSEADEKHP-----
674 -----DVNSVHSKRDSSERRPD SAYSTS KDTKRYOSVVVVISDEKDECIIA 718	674 -----DVNSVHSKRDSSERRPD SAYSTS KDTKRYOSVVVVISDEKDECIIA 718
RESULT 11	RESULT 11
P87357 PRELIMINARY; PRT; 717 AA.	P87357 PRELIMINARY; PRT; 717 AA.
ID P87357; AC P87357;	ID P87357; AC P87357;
DT 01-MAY-1997 (TREMBLrel. 03, Created)	DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)	DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Delta transmembrane protein precursor.	DE Delta transmembrane protein precursor.
GN Name=dld; Synonyms=deltaD;	GN Name=dld; Synonyms=deltaD;
OS Brachydanio rerio (Zebrafish) (Danio rerio).	OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysii; Cypriniformes;	OC Actinopterygii; Neopterygii; Teleostei; Ostariophysii; Cypriniformes;
OC Cyprinidae; Danio.	OC Cyprinidae; Danio.
NCBI_TaxID=7955;	NCBI_TaxID=7955;
[1] RSEQUENCE FROM N.A. RP SEQUENCE FROM N.A.	[1] RSEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
RX MEDLINE=97346722; PubMed=9203139; RA Dornseifer P., Takke C., Campos-Ortega J.A.;	RX MEDLINE=97346722; PubMed=9203139; RA Dornseifer P., Takke C., Campos-Ortega J.A.;
RT "Overexpression of a Delta homologue of the Drosophila neurogenic gene delta perturbs differentiation of primary neurons and somitic development." ; DR EMBL; Y11760; CAA72425.1; - .	RT "Overexpression of a Delta homologue of the Drosophila neurogenic gene delta perturbs differentiation of primary neurons and somitic development." ; DR EMBL; Y11760; CAA72425.1; - .
RL GO; GO:0005509; F:calcium ion binding; IEA.	RL GO; GO:0005509; F:calcium ion binding; IEA.
DR ZFIN; ZDB-GENE-990415-47; dld.	DR ZFIN; ZDB-GENE-990415-47; dld.
DR InterPro; IPR000152; Abx_hydroxyl_S.	DR InterPro; IPR000152; Abx_hydroxyl_S.
SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.	SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
RX MEDLINE=95319507; PubMed=7596411; RA Henriques D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;	RX MEDLINE=95319507; PubMed=7596411; RA Henriques D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
RT "Expression of a Delta homologue in prospective neurons in the chick." ; RT Nature 375:787-790(1995).	RT "Expression of a Delta homologue in prospective neurons in the chick." ; RT Nature 375:787-790(1995).
RL NCBI_TaxID=8355;	RL NCBI_TaxID=8355;
[2] RSEQUENCE FROM N.A. RP SEQUENCE FROM N.A.	[2] RSEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
RX MEDLINE=95319503; PubMed=7596407; RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;	RX MEDLINE=95319503; PubMed=7596407; RA Chitnis A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
RT GO; GO:0005509; P:cell communication; IEA.	RT GO; GO:0005509; P:cell communication; IEA.
DR InterPro; IPR000152; Abx_hydroxyl_S.	DR InterPro; IPR000152; Abx_hydroxyl_S.

-!- SIMILARITY: Contains 8 EGF-like domains.

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CC DR EMBL; AF253468; AAF76427.1; .

CC DR EMBL; ABO36931; BAB16085.1; .

CC DR EMBL; ABO43894; BAB18581.1; .

CC DR EMBL; AY358894; AAQ89253.1; .

CC DR EMBL; AF279305; AAF81912.1; .

CC DR PIR; JC7570; JC7570.

CC DR HSSP; P00740; 1EDM.

CC DR Genew; HGNC; 2910; DLL4.

CC DR MIM; 605185; .

CC DR GO; GO:0005112; F:Notch binding; TAS.

CC DR GO; GO:0008015; P:circulation; TAS.

CC DR GO; GO:0007165; P:signal transduction; TAS.

CC DR InterPro; IPR001152; ASX_hydroxyl_S.

CC DR InterPro; IPR001774; DSL.

CC DR InterPro; IPR000742; EGF_2.

CC DR InterPro; IPR001438; EGF_III.

CC DR InterPro; IPR006209; EGF-like.

CC DR Pfam; PF01414; DSL_1.

CC DR Pfam; PF000008; EGF_7.

CC DR PRINTS; PRO00010; EGFBLOOD.

CC DR PROSITE; PS00010; ASX_HYDROXYL_1.

CC DR PROSITE; PS00022; EGF_1; 8.

CC DR PROSITE; PS01186; EGF_2; 7.

CC DR PROSITE; PS55026; EGF_3; 8.

KW Developmental protein; Differentiation; Direct protein sequencing;

KW EGF-like domain; Glycoprotein; Repeat; Signal; Transmembrane.

FT SIGNAL 1 26

FT CHAIN 27 685 Delta-like protein 4.

FT DOMAIN 27 529 Extracellular (Potential).

FT TRANSMEM 530 550 Potential.

FT DOMAIN 551 685 Cyttoplasmic (Potential).

FT DOMAIN 218 251 DSL.

FT DOMAIN 252 282 EGF-like 1.

FT DOMAIN 284 322 EGF-like 2.

FT DOMAIN 324 360 EGF-like 3.

FT DOMAIN 362 400 EGF-like 4.

FT DOMAIN 402 438 EGF-like 5.

FT DOMAIN 440 476 EGF-like 6.

FT DOMAIN 480 518 EGF-like 7.

FT DISULFID 222 233 EGF-like 8.

FT DISULFID 226 239 By similarity.

FT DISULFID 241 250 By similarity.

FT DISULFID 253 264 By similarity.

FT DISULFID 259 270 By similarity.

FT DISULFID 272 281 By similarity.

FT DISULFID 288 300 By similarity.

FT DISULFID 294 310 By similarity.

FT DISULFID 312 321 By similarity.

FT DISULFID 328 339 By similarity.

FT DISULFID 333 348 By similarity.

FT DISULFID 350 359 By similarity.

FT DISULFID 366 377 By similarity.

FT DISULFID 371 388 By similarity.

FT DISULFID 390 399 By similarity.

FT DISULFID 406 417 By similarity.

FT DISULFID 411 426 By similarity.

FT DISULFID 428 437 By similarity.

FT DISULFID 444 464 By similarity.

FT DISULFID 466 475 By similarity.

FT DISULFID 484 495 By similarity.

FT DISULFID 489 506 By similarity.

FT DISULFID 508 517 By similarity.

CC Query Match 13.7%; Score 126.5; DB 1; Length 685;

CC Best Local Similarity 26.7%; Pred. No. 0.001;

CC Matches 47; Conservative 23; Mismatches 43; Indels 63; Gaps 7;

CC Qy 2 MNMLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQDL 61

CC Db 568 MNMLNSDFQKD-----NLIPAAQLKNTNQKKELEV-DCGIDDKSNCGKQQNHTLDYNL---- 617

CC Qy 62 KGDDTAVRTSHSKRDTKCQSPGSSGR--RRGPRPHSGXACCGPGSGGTWGVSWNHCSV 119

CC Db 618 -----APGPLGRGTMPPGKFPHSDKSL-----GEKAPRLH 648

CC Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDGCSTSNDTKYQSVYVISSEEKDECVIA 175

CC Db 649 EKPBC-----RISAICS-PRDSMYQSVCLISSEERNECVIA 682

Search completed: December 2, 2004, 04:01:22

Job time : 196 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2004, 03:52:42 ; Search time 39 Seconds
(without alignments)
431.742 Million cell updates/sec

Title: US-09-783-931-23
Perfect score: 926
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSYYVISEEKDECYIA 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	428	46.2	722	2 I48324	DELTA-like 1 - mouse
2	388	41.9	728	2 I50719	C-Delta-1 - chicken
3	126.5	13.7	685	2 JC7570	Delta-4 protein -
4	125.5	13.6	686	2 JC7569	Delta-4 protein -
5	88.5	9.6	1106	1 TVHUGL	transforming prote
6	87.5	9.4	925	2 T29311	hypothetical prote
7	86.5	9.3	504	2 T13475	hypothetical prote
8	83.5	9.0	1651	2 T14160	transmembrane rece
9	83	9.0	1707	2 T18951	hypothetical prote
10	81	8.7	763	2 AC0108	probable primate Y
11	79.5	8.6	326	2 A41732	heterogeneous ribo
12	79.5	8.6	386	1 S22315	snRNP-associated p
13	78.5	8.5	512	2 T47793	receptor-like prot
14	77.5	8.4	538	2 T49418	hypothetical prote
15	77.5	8.4	929	2 C96623	transcription fact
16	77.5	8.5	8.2	2 D41602	hypothetical prote
17	75.5	8.2	435	2 F84849	transcription fact
18	75.5	8.2	1191	2 T13850	gene u-shaped prot
19	75.5	8.2	1433	2 A46053	bulous pemphigoid
20	75.5	8.2	1612	2 T30805	duttl protein - mo
21	75.5	8.2	424	2 T41449	probable phd finge
22	75	8.1	439	1 A48099	transcription fact
23	75	8.1	282	2 S78141	ribosomal protein
24	74.5	8.0	367	2 AD0404	probable sugar ABC
25	74	8.0	1464	2 S58984	development protei
26	74	8.0	1613	2 T06678	hypothetical prote
27	74	7.9	154	2 A33896	isotocin 1 / neuro
28	73.5	7.9	376	2 G96579	hypothetical prote

A;Residues: 1-728 <HEN>
A;Cross-references: UNIPROT:Q90656; EMBL:U26590; NID:g882411; PIDN:AAC59689.1; PMID:98824
C;Superfamily: delta-4 protein; EGF homology
F;299-332/Domain: EGF homology <EGX1>
F;339-370/Domain: EGF homology <EGF1>
F;416-447/Domain: EGF homology <EGX2>
F;454-485/Domain: EGF homology <EGF>
F;492-523/Domain: EGF homology <EGF3>

Query Match 41.9%; Score 388; DB 2; Length 728;
Best Local Similarity 49.7%; Pred. No. 7.2e-30;
Matches 87; Conservative 15; Mismatches 27; Indels 46; Gaps 5;

Qy 1 TMNLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
Db 597 TMNLANCOREKDISVIGATQIKNTNKVKDFH--SDNSDKNGY-KVRYPSVDYNLVHE 653

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRGGPRPHSGXACCGPGSGGGTWGVSSWNHCVS 120
Db 654 LKNED-SVKEEHGKCEAKCETYDSEAEKS-----AVQ 685

Qy 121 LPKCSHAIFIIVDFLYPFPSGEASERKRPDSGCSTSNDTKYQSVVYVISEEKDECVIA 175
Db 686 LK-----SSDTSERKRPDSVYSTSKDTKYQSVVYVISEEKDECIIA 725

RESULT 3
JC7570 Delta-4 protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7570
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Accession: JC7570
A;Molecule type: mRNA
A;Residues: 1-685 <YON>
A;Cross-references: UNIPROT:Q9NR61; DDBJ:AB043894
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane receptor the Notch signaling, the growth or differentiation of vascular endothelial cells.
C;Genetics:
A;Gene: delta-4
C;Superfamily: delta-4 protein; EGF homology
C;Keywords: transmembrane protein

Query Match 13.7%; Score 126.5; DB 2; Length 685;
Best Local Similarity 26.7%; Pred. No. 0.0002; Mismatches 43; Indels 63; Gaps 7;

Qy 2 MNLLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 61
Db 568 MNLLNSDFQKD----NLIPAAQLKNTNQKKELEV-DCGLDKSNCGKQQNHTLDYNL--- 617

Qy 62 KGDDTAVRTSHSKRDTKCQSPGSSGR--RKGPRPHSGXACCGPGSGGGTWGVSSWNHCVS 119
Db 618 -----APGLIGRTMPGKFPHSDKSL-----GEKAPRLHS 648

Qy 120 SLPKCSHAIFIIVDFLYPFPSGEASERKRPDSGCSTSNDTKYQSVVYVISEEKDECVIA 175
Db 649 EKPEC-----RISAIICS-PRDSMYQSVCILSEERNECVIA 682

RESULT 4
JC7569 Delta-4 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7569
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Osawa, M.; Miyatani, S.;
J. Biochem. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.

A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Accession: JC7569
A;Molecule type: mRNA
A;Residues: 1-686 <YON>
A;Cross-references: UNIPROT:Q9DBU9; DDBJ:AB043893
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane receptor the Notch signaling, the growth or differentiation of vascular endothelial cells.
C;Genetics:
A;Gene: delta-4
C;Superfamily: delta-4 protein; EGF homology

Query Match 13.6%; Score 125.5; DB 2; Length 686;
Best Local Similarity 24.9%; Pred. No. 0.00025; Mismatches 43; Indels 65; Gaps 6;
Matches 44; Conservative 25; Mismatches 43; Indels 65; Gaps 6;

Qy 2 MNLLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 61
Db 569 MNLLNSDFQKD----NLIPAAQLKNTNQKKELEV-DCGLDKSNCGKQQNHTLDYNLAPGL 622

Qy 62 KGDDTAVRTSHSKRDTKCQSPGSSGRGGPRPHSGXACCGPGSGGGTWGVSSWNHCVS 121
Db 623 LG-----RGGMGPCKYPHPDKS-----LGEKV 643

Qy 122 PKCSHAIFIIVDFLYPFPSGEASERKRPD---SGCSTSNDTKYQSVVYVISEEKDECVIA 175
Db 644 PLRLHS-----EKPECRIAIICSPRDSMYQSVCILSEERNECVIA 683

RESULT 5
TVHUGL transforming protein gli - human
N;Alternate names: glioma-associated transforming protein
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: S00672
R;Kinzler, K.W.; Ruppert, J.M.; Bigner, S.H.; Vogelstein, B.
Nature 332, 371-374, 1988
A;Title: The GLI gene is a member of the Kruppel family of zinc finger proteins.
A;Reference number: S00672
A;Accession: S00672
A;Molecule type: mRNA
A;Residues: 1-1106 <KIN>
A;Cross-references: UNIPROT:P08151; EMBL:X07384; NID:931767; PIDN:CAA30297.1; PID:931768
C;Genetics:

A;Gene: GDB:GLI
A;Cross-references: GDB:119988; OMIM:165220
A;Map position: 12q13.2-12q13.3
C;Superfamily: Glii transforming protein
C;Keywords: DNA binding; duplication; oncogene; transcription regulation; transforming protein
F;235-260/Region: zinc finger CCHH motif
F;268-295/Region: zinc finger CCHH motif
F;301-325/Region: zinc finger CCHH motif
F;331-356/Region: zinc finger CCHH motif
F;362-387/Region: zinc finger CCHH motif

Query Match 9.6%; Score 88.5; DB 1; Length 1106;
Best Local Similarity 21.8%; Pred. No. 1.7; Mismatches 24; Indels 65; Gaps 8;
Matches 42; Conservative 24; Mismatches 24; Indels 65; Gaps 8;

Qy 39 SSDRKGFQKARYPSVDYNLVQDLKG-DTAVRTSHSKR-----DTKCGQSPGSS----- 85
Db 69 SSPRSAVKLTKRALSISPLSDASLDLQTVRTPSSLLVAFINSRCTSPGGSYGHLSIGT 128

Qy 86 -----GRRRGPRPHSGXACCGP-GSGGGTWGVSSWNHCVS 133
Db 129 MPSLGLFPAPAQMNHQKG-----GMI PHPQSRGPFPPTCQLKSELDML 186

Qy 134 Y-----PPFSEAS-----ERKRPD-----GCSTSK 155
Db 187 VGKCREEPLEGDMSSPNSTGIQDPILLGMLDREDLEREKREPESEVYETDCRWDGCSQEF 246

Qy 156 DTKQSVVYVISEE 168

Query Match 8.5%; Score 78.5; DB 2; Length 512;
 Best Local Similarity 26.2%; Pred. No. 7.1;
 Matches 32; Conservative 7; Mismatches 54; Indels 29; Gaps 4;

Qy 12 KDISVSIIGATGIXNTNKKADFXGDXSSDNGFQKARYPSVDYNNVQDLKGDDTAVRTS 71
 Db 72 KDIRVD-DRVGFQNHNENLISITNAKSSDRNSGKMMSYLG----RTK 113

Qy 72 HSKRDTKCQSPGSSGRRGPRHSGXACCGPGSGGGTWCVSSNHCS----VSLPKC 124
 Db 114 SSDNDSISQCSSSVHHHERACSSHSGE---DGSGFAAWRQNSLSQQGLVTASPLVGLPEI 169

Qy 125 SH 126
 Db 170 SH 171

RESULT 14

T49418 hypothetical protein B1D4.330 [Imported] - Neurospora crassa
 C;Species: Neurospora crassa
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T49418
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, May 2000
 A;Reference number: Z25022
 A;Accession: T49418
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-538 <SCH>
 A;Cross-references: UNIPROT:O9P649; EMBL:AL355928; GSPDB:GN00116; NCSP:B1D4.330
 A;Experimental source: BAC clone B1D4; Strain OR74A
 C;Genetics:

A;Gene: B1D4.330
 A;Map position: 6
 A;Introns: 162/2

Query Match 8.4%; Score 77.5; DB 2; Length 538;
 Best Local Similarity 24.0%; Pred. No. 9.3;
 Matches 35; Conservative 18; Mismatches 48; Indels 45; Gaps 9;

Qy 46 QKARYPSVDYNNVQDLKGDDTAVRTSHSKRDTKQCSPGSSGRR-----RGPRLPHSGX 97
 Db 95 QHAQYQ---HYHAV---TGDNKKATTKRAKRHRGP-EAPGGEGRKFAACPFCQHNPARYRTVK 148

Qy 98 ACCGPGGGGTWGV-----SSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERK 145
 Db 149 TCCGPG-----WDSVHRVKEHYRRHSLKNTC----PRCYDQFKTD-----DDLKRHQ 192

Qy 146 RPDSGCSTSCKDTKYQSVVYISEEKDE 171
 Db 193 RAETPCRLRKDNDVPE---VITDEQDK 215

RESULT 15

C96623 hypothetical protein F23H11.22 [Imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: C96623
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurois, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: C96623
 A;Status: preliminary

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OM protein - protein search, using sw model

Run on: December 2, 2004, 04:01:28 ; Search time 3243 Seconds
(without alignments)
19.244 Million cell updates/sec

Title: US-09-783-931-23

Perfect score: 926

Sequence: 1 TMNLANCQREKDISVSIIG.....DTKYQSYYVISEEKDECVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$

Maximum Match 100*

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
1	916	98.9	175	9 US-09-908-322-23 Sequence 23, Appl
2	916	98.9	175	10 US-09-908-322-23 Sequence 23, Appl
3	631.5	68.2	118	9 US-09-908-322-17 Sequence 17, Appl
4	631.5	68.2	118	10 US-09-908-322-17 Sequence 17, Appl
5	527.5	57.0	702	9 US-09-995-593A-4 Sequence 4, Appl
6	527.5	57.0	723	9 US-09-828-366-21 Sequence 21, Appl
7	527.5	57.0	723	9 US-09-995-593A-9 Sequence 9, Appl
8	527.5	57.0	723	14 US-10-028-072-346 Sequence 346, App
9	527.5	57.0	723	14 US-10-140-808-346 Sequence 346, App
10	527.5	57.0	723	14 US-10-121-049-346 Sequence 346, App
11	527.5	57.0	723	14 US-10-123-904-346 Sequence 346, App
12	527.5	57.0	723	14 US-10-140-470-346 Sequence 346, App
13	527.5	57.0	723	14 US-10-175-746-346 Sequence 346, App

RESULT 1
US-09-908-322-23
; Sequence 23, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-JUL-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S Leslie
; REGISTRATION NUMBER: 18, 872
; REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids

TYPE: amino acid
 STRANDEDNESS: <Unknown>

TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-783-931-23

Query Match 98.9%; Score 916; DB 9; Length 175;

Best Local Similarity 100.0%; Pred. No. 2.6e-86;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADEFXXGDXSSDKNGFQKARYPSVDYNLVQD 60

Db 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADEFXXGDXSSDKNGFQKARYPSVDYNLVQD 60

Qy 1 LKGDDTAVRTSHSKRDTKQSPGSGRRRGPRPHSGXACCGPGSGGGTWGVSSWNHCSV 120

Db 1 LKGDDTAVRTSHSKRDTKQSPGSGRRRGPRPHSGXACCGPGSGGGTWGVSSWNHCSV 120

Qy 61 LPKCASHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVVVISSEEKDECVIA 175

Db 61 LPKCASHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTKYQSVVVISSEEKDECVIA 175

RESULT 3

US-09-908-322-17

Sequence 17, Application US/09908322

Patent No. US20020107194A1

GENERAL INFORMATION:

APPLICANT: Ish-Horowicz, David Pinto

Lewis, Julian Hart

Artavanis-Tsakonas, Spyridon

Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/908,322

FILING DATE: 22-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-123

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

US-09-908-322-17

Query Match 68.2%; Score 631.5; DB 9; Length 118;
Best Local Similarity 99.2%; Pred. No. 3.8e-57;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 57 LvQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACCGPGSGGGTGWGVSSWNH 116
1 LvQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACCGPGSGGGTGWGVSSWNH 59

Query Match 117 CSVSLPKCSHAFIVDFLYFPFSEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 175
Db 60 CSVSLPKCSHAFIVDFLYFPFSEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 118

RESULT 5
US-09-995-593A-4
; Sequence 4, Application US/09995593A
; Patent No. US20020128197A1
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; INVENTOR: ITOH, AKIRA
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP8447DIV
; CURRENT APPLICATION NUMBER: US/09/995,593A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 09/068,740
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: JP 7-299611
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: JP 7-311811
; PRIOR FILING DATE: 1995-11-30
; PRIOR APPLICATION NUMBER: PCT/JPP96/03356
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-995-593A-4

Query Match 57.0%; Score 527.5; DB 9; Length 702;
Best Local Similarity 64.8%; Pred. No. 1.8e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Db 1 TMMNLANCQREKDVSIIAGATGIXNTNKKADEXXGDXSSDKNGFQKARYPSVDYNLVQD 60
568 TMMNLANCQREKDVSIIAGATQIKNTNKKADEP-HGDHSADKNGF-KARYPAVDYNLVQD 625

Query Match 61 LKGDDTAVRTSHSKRDTKCCSPGSSGRRRG-PRPHSGXACCGPGSGGGTGWGVSSWNHCSV 119
Db 626 LKGDDTAVRDAHSKRDTKCOPQSSGEEKGTPTRLRQ----- 662

Query Match 120 SLPKCSHAFIVDFLYFPFSEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 175
Db 663 -----GEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 699

RESULT 6
US-09-828-366-21
; Sequence 21, Application US/09828366
; Patent No. US2002010137A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; INVENTOR: Ashkenazi, Avi
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klein, Robert D.
; APPLICANT: Napier, Mary
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P1694R1C1
; CURRENT APPLICATION NUMBER: US/09/828,366
; CURRENT FILING DATE: 2001-04-05
; Prior filing data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 21
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapien

Query Match 68.2%; Score 631.5; DB 10; Length 118;
Best Local Similarity 99.2%; Pred. No. 3.8e-57;
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 57 LvQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACCGPGSGGGTGWGVSSWNH 116
1 LvQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACCGPGSGGGTGWGVSSWNH 59

US-09-828-366-21

Query Match	Score	DB	Length
Best Local Similarity	57.0*	9	723
Matches	64.8*	Pred. No.	1.8e-45;
Matches	114;	Conservative	4; Mismatches
			13; Indels
			45; Gaps
			4;

1 TMNNLANCOREKDIISSIIIGATGIXNTNKKADFXXGDXSSDKNGFQKARYPSVDXNLVQD 60

Query Match 57.0%; Score 527.5; DB 9; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKDNGFQKARYPSVDYNLVQD 60
 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADDF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQQPQGSSEEKGTPPTTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCSTSKDTKYQSVVVISEEKDECVIA 175
 Db 684 -----GEASERKRPDSCGCSTSKDTKYQSVVVISEEKDECVIA 720

RESULT 7
 US-09-995-593A-9
 Sequence 9, Application US/09995593A
 Patent No. US20020128197A1
 GENERAL INFORMATION:
 APPLICANT: SAKANO, SEIJI
 APPLICANT: ITOH, AKIRA
 TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
 FILE REFERENCE: KP8447DIV
 CURRENT APPLICATION NUMBER: US/09/995,593A
 CURRENT FILING DATE: 2002-02-28
 PRIOR APPLICATION NUMBER: 09/068,740
 PRIOR FILING DATE: 1998-06-18
 PRIOR FILING DATE: JP 7-299611
 PRIOR APPLICATION NUMBER: 1995-11-17
 PRIOR FILING DATE: JP 7-311811
 PRIOR FILING DATE: 1995-11-30
 PRIOR APPLICATION NUMBER: PCT/JP96/03356
 PRIOR FILING DATE: 1996-11-15
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 9
 LENGTH: 723
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-995-593A-9

Query Match 57.0%; Score 527.5; DB 9; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXGDXSSDKDNGFQKARYPSVDYNLVQD 60
 589 TMNNLANCQREKDISVSIIGATQIKNTNKKADDF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRRG-PRPHSGXACCGPGSGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQQPQGSSEEKGTPPTTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCGCSTSKDTKYQSVVVISEEKDECVIA 175
 Db 684 -----GEASERKRPDSCGCSTSKDTKYQSVVVISEEKDECVIA 720

RESULT 8
 US-10-028-072-346
 Sequence 346, Application US/10028072
 Publication No. US20030004311A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Trumas, Daniel
 APPLICANT: Watanabe, Colin K

PRIOR APPLICATION NUMBER: 60/0855579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086414
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/086430
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088730
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088741
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090538
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1. Be-45;
 Matches 114; Conservative 4; Mismatches 13; Indel 8 4;
 Gap 4;

Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLQD 60
Db	589 TMNNLANCOREKDISVSIIGATQIRNTNKKADF-HGDHSADDQNGF-KARYPAVDYNLQD 646
Qy	61 LKGDDTAVRTSHSKRDTKQCSPGSGRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV 119
Db	647 LKGDDTAVRDAHSKRDTKQCPOGSSEEKGTPPTLRG-- 683
Qy	120 SLPKCSHAFIVDFLYPPFSGEASERKRPDSGCSTS KDTKYQSYYSEEKDECYIA 175
Db	684 ---GEASERKRPDSGCSTS KDTKYQSYYSEEKDECYIA 720

RESULT 9
 US-10-140-808-346
 Sequence 346, Application US/10140808
 Publication No. US20030017563A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C182
 ; CURRENT APPLICATION NUMBER: US/10/140,808
 ; CURRENT FILING DATE: 2002-05-07
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 346
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-808-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

RESULT 11
 US-10-123-904-346
 ; Sequence 346, Application US/10123904
 ; Publication No. US20030022328A1

; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C54
 ; CURRENT APPLICATION NUMBER: US/10/123,904
 ; CURRENT FILING DATE: 2002-04-16
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 346
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-123-904-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

RESULT 10
 US-10-121-049-346
 ; Sequence 346, Application US/10121049
 ; Publication No. US2003002239A1

; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

RESULT 11
 US-10-123-904-346
 ; Sequence 346, Application US/10123904
 ; Publication No. US20030022328A1

; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C54
 ; CURRENT APPLICATION NUMBER: US/10/123,904
 ; CURRENT FILING DATE: 2002-04-16
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 346
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-123-904-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

RESULT 12
 US-10-123-904-346
 ; Sequence 346, Application US/10123904
 ; Publication No. US20030022328A1

; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

RESULT 12
 US-10-140-470-346
 ; Sequence 346, Application US/10140470
 ; Publication No. US20030022331A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C160
 ; CURRENT APPLICATION NUMBER: US/10/140,470
 ; CURRENT FILING DATE: 2002-05-06
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 346
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-470-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADDFXXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADDF-HGDHSADKNGF-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKQCSPGSSGRRRG-PRPHSGXACCGPGSGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRTSHSKRDTKQCQPQGSGBEKGTPTTLRG----- 683

Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSCSTSKEKTYQSVVVISEEKDECIVIA 175
 Db 684 -----GEASERKRPDSCSTSKEKTYQSVVVISEEKDECIVIA 720

RESULT 14

US-10-176-918-346

; Sequence 346, Application US/10176918
 ; Publication No. US20030027275A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C382
 ; CURRENT APPLICATION NUMBER: US/10/176,918
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 346
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-918-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;

Best Local Similarity 64.8%; Pred. No. 1.8e-45;

Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADDFXXGDXSSDKNGFQKARYPSVDYNLVQD 60

Db 589 TMNLANCOREKDISVSIIGATIQKNTNKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 Qy 61 LKGDDTAVRTSHSKRDTKCQSGSSGRRG-PRPHSGXACCGPGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRTDAHSKRDTKCQPQGSSGEEKGTPPTLRG----- 683
 Qy 120 SLPKCSHAFAIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 175
 Db 684 -----GEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 720

RESULT 15
 US-10-176-921-346
 / Sequence 346, Application US/10176921
 / Publication No. US20030027276A1
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Beresini, Maureen
 / APPLICANT: DeForge, Laura
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Sherwood, Steven
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watanabe, Colin K
 / APPLICANT: Wood, William
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / ACIDS ENCODING THE SAME
 / FILE REFERENCE: P3330R1C288
 / CURRENT APPLICATION NUMBER: US/10/176,921
 / CURRENT FILING DATE: 2002-06-20
 / Prior Application removed - See File wrapper or Palm
 / NUMBER OF SEQ ID NOS: 550
 / SEQ ID NO 346
 / LENGTH: 723
 / TYPE: PRT
 / ORGANISM: Homo Sapien
 US-10-176-921-346

Query Match 57.0%; Score 527.5; DB 14; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.8e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNLANCOREKDISVSIIGATIGIXNTNKADFXXXDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNLANCOREKDISVSIIGATIQKNTNKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 Qy 61 LKGDDTAVRTSHSKRDTKCQSPGSSGRRG-PRPHSGXACCGPGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRTDAHSKRDTKCQPQGSSGEEKGTPPTLRG----- 683
 Qy 120 SLPKCSHAFAIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 175
 Db 684 -----GEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 720

Search completed: December 2, 2004, 05:08:08
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26 ADA76296 Human PRO
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28 ADA61569 Homo sapi
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32 527.5 57.0 723 6 ADB15938
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26 2002273 seqs, 358729299 residues

27 2002273 seqs, 358729299 residues

28 2002273 seqs, 358729299 residues

29 2002273 seqs, 358729299 residues

30 2002273 seqs, 358729299 residues

31 2002273 seqs, 358729299 residues

32 2002273 seqs, 358729299 residues

33 2002273 seqs, 358729299 residues

34 2002273 seqs, 358729299 residues

35 2002273 seqs, 358729299 residues

36 2002273 seqs, 358729299 residues

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44 2002273 seqs, 358729299 residues

45 2002273 seqs, 358729299 residues

Run on: December 2, 2004, 03:51:27 ; Search time 153 Seconds
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410.311 Million cell updates/sec

Title: US-09-783-931-23

Perfect score: 926

Sequence: 1 TMNQLANCQREKDISVSIIG.....DTKYQSVVVSEEKDECVIA 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

כונתנו וענינו

RESULT 1
 AAW11724
 ID AAW11724 standard; protein; 175 AA.
 XX
 AC AAW11724;
 XX
 DT 28-APR-1997 (first entry)
 XX
 DE H-Delta-1 polypeptide predicted sequence.
 XX
 KW H-Delta-1; cell proliferation; nervous system disorder;
 tissue regeneration; Notch; cervix cancer; breast cancer;
 colon cancer; melanoma; seminoma; neurogenesis; therapy.
 KW
 KW
 KW

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IMMAPTES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	908	98.1	175	2	AAW	11724	H-Delta-1
2	678.5	73.3	175	2	AAW	11721	H-Delta-1
3	527.5	57.0	702	2	AAW	18349	Prolifera
4	527.5	57.0	702	2	AAW	75495	Truncated
5	527.5	57.0	723	2	AAW	18353	Prolifera
6	527.5	57.0	723	2	AAW	75492	Human del
7	527.5	57.0	723	2	AAW	94498	Human del
8	527.5	57.0	723	3	AAY	83227	PRO172 Po
9	527.5	57.0	723	3	AAB	33422	Human PRO
10	527.5	57.0	723	3	AAB	24388	Human PRO
11	527.5	57.0	723	3	AAY	79032	Human del
12	527.5	57.0	723	3	AAB	00172	PRO172 po
13	527.5	57.0	723	4	AAU	12344	Human PRO
14	527.5	57.0	723	4	AAB	53064	Human ang
15	527.5	57.0	723	6	ABO	17788	Novel hum
16	527.5	57.0	723	6	ABU	81042	Human PRO
17	527.5	57.0	723	6	ABP	97824	Amino aci
18	527.5	57.0	723	6	ABU	66742	Human PRO
19	527.5	57.0	723	6	ABU	55879	Human not
20	527.5	57.0	723	6	AAE	34035	Human not
21	527.5	57.0	723	6	ABU	59823	Novel sec
22	527.5	57.0	723	6	ABO	25013	Human sec
23	527.5	57.0	723	6	ABP	72566	Human Not
24	527.5	57.0	723	6	ABU	67018	Human sec
25	527.5	57.0	723	6	ADA	45865	Novel hum

PS Claim 41; Fig 11; 135pp; English.

XX The amino acid sequence (AAW11724) of H-Delta-1 was predicted by
 CC alignment of polypeptides (AAW11721-23) corresponding to the 3 reading
 CC frames of an isolated H-Delta-1 gene sequence (AAT58900) with that of
 CC chick C-Delta-1 (AAW58897). Because of sequencing errors in the gene
 CC sequence, the homology was obtnd. by switching amongst the 3 open reading
 CC frames to identify homologous regions. H-Delta-1 polypeptide sequences
 CC (AAW11725-38) were also deduced from a contig sequence (AAT59454). H-
 Delta-1 is the human homologue of the Drosophila Delta protein that binds
 CC to Notch protein. H-Delta-1 polypeptides can be used to treat or prevent
 CC disorders characterised by increased Notch activity, such as cervical,
 CC breast, lung or colon cancer, melanoma or seminoma, as well as nervous
 CC system disorders, and to promote tissue regeneration and repair

XX SQ Sequence 175 AA;

Query Match 98.1%; Score 908; DB 2; Length 175;
 Best Local Similarity 99.4%; Pred. No. 9.9e-86;
 Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TMNNILANCQREKDISVSIIGATIXNTNKKADFXGDXSSDKNGFQKARYPSVDYQNLVQD 60
 Db 1 TMNNILANCQREKDISVSIIGATIXNTNKKADFXGDXSSDKNGFQKARYPSVDYQNLVQD 60

Qy 61 LKGDDTAVRTSHSKRDTKQSPGSSGRGGPRPHSGXACCGPGSGGGTWGVSSWNHCSV 120
 Db 61 LKGDDTAVRTSHSKRDTKQSPGSSGRGGPRPHSGXACCGPGSGGGTWGVSSWNHCSV 120

Qy 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSSGCSTSKEKTYQSVTYVISEEKDECYIA 175
 Db 121 LPKCSHAFIVDFLYFPFSGEASERKRPDSSGCSTSKEKTYQSVTYVISEEKDECYIA 175

RESULT 2
 AAW11721 ID AAW11721 standard; protein; 175 AA.
 XX AC AAW11721;
 XX DT 28-APR-1997 (first entry)
 XX DE H-Delta-1 polypeptide (reading frame 1 product).

XX H-Delta-1; cell proliferation; nervous system disorder;
 KW tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer;
 KW colon cancer; melanoma; seminoma; neurogenesis; therapy.

OS Homo sapiens.

XX Key Location/Qualifiers
 FT Misc-difference 4
 FT /label= Gln, Stop
 /note= "variable site resulting from degeneracy of the H-
 delta-1 DNA sequence"
 FT Misc-difference 22
 FT /label= Tyr, His
 /note= "variable site resulting from degeneracy of the H-
 delta-1 DNA sequence"
 FT Misc-difference 26
 FT /label= Arg, Gly
 /note= "variable site resulting from degeneracy of the H-
 delta-1 DNA sequence"
 FT Misc-difference 34
 FT /label= His, Gln
 /note= "variable site resulting from degeneracy of the H-
 delta-1 DNA sequence"
 FT Misc-difference 35
 FT /label= Ser, Arg
 /note= "variable site resulting from degeneracy of the H-
 delta-1 DNA sequence"

FT Misc-difference 56
 FT /note= "residue 50 corresponds to a stop codon in the H-
 delta-1 DNA sequence"
 FT Misc-difference 97
 FT /label= Gly, Val
 /note= "variable site resulting from degeneracy of the H-
 delta-1 DNA sequence"
 XX WO9701571-A1.
 XX PD 16-JAN-1997.
 XX PF 28-JUN-1996; 96WO-US011178.
 XX PR 28-JUN-1995; 95US-0000589P.
 XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA (UYA) UNIV YALE.
 XX PI Ish-Horowicz D, Henrique D, Lewis J, Artavanis-Tsakonas S;
 PI Gray GE;
 XX DR WPI: 1997-100159/09.
 DR N-PSDB; AAT58900.
 XX PT New vertebrate Delta protein, DNA and antibodies - for treating and
 preventing cancer, nervous system disorders and for tissue regeneration.
 XX PS Disclosure; Fig 10A-B; 135pp; English.
 XX CC Polypeptide sequences (AAW11721-23) were detd. for all 3 reading frames
 CC of a human H-Delta-1 gene sequence (AAT58900) isolated from a genomic
 CC library. No single reading frame gave the correct sequence owing to
 CC errors that caused reading frameshifts. An alignment of the polypeptides
 CC with that of chick C-delta-1 (AAW11719) allowed the correct H-Delta-1
 CC sequence to be predicted (see also AAW11724). H-Delta-1 polypeptide
 CC sequences (AAW11725-38) were also deduced from an H-Delta-1 contig
 CC (AAT59454). Delta-1 proteins can be used to treat or prevent disorders
 CC characterised by increased Notch activity, such as cervical, breast, lung
 CC or colon cancer, melanoma or seminoma, as well as nervous system
 CC disorders, and to promote tissue regeneration and repair
 XX SQ Sequence 175 AA;

Query Match 73.3%; Score 678.5; DB 2; Length 175;
 Best Local Similarity 92.1%; Pred. No. 6.1e-62;
 Matches 129; Conservative 1; Mismatches 9; Indels 8; Gaps 1;

Qy 36 GDXSSDKNGFQKARYPSVDYQNLVQDLKGDDTAVRTSHSKRDTKQSPGSSGRGGPRPHS 95
 Db 37 GTXASDQNGFQ-GPLPQRGLXLVQDLKGDDTAVRTSHSKRDTKQSPGSSGRGGPRPHS 95

Qy 96 GXACCGPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSSGCSTS 155
 Db 96 GXACCGPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSSGCSTS 155

Qy 156 DTKYQSVVVISSEKDECYIA 175
 Db 156 DTKYQSVVVISSEKDECYIA 175

RESULT 3
 AAW18349 ID AAW18349 standard; protein; 702 AA.
 XX AC AAW18349;
 XX DT 11-FEB-1998 (first entry)
 XX DE Proliferation and differentiation suppression polypeptide.
 XX KW

KW	blood cell; neuron; leukaemia; malignant tumour; immunosuppression.	PA	(ASAHI) ASAHI KASEI KOGYO KK.
XX		XX	
OS	Homo sapiens.	DR	1999-076401/07.
XX		XX	
WO9719172-A1.	Vascular cell controlling agent comprises polypeptide - which is human	PT	
XX	notch ligand and is used as drug.	PT	
PD		XX	
29-MAY-1997.	Claim 2; Page 14-16; 21pp; Japanese.	PS	
XX		XX	
PF	15-NOV-1996;	96WO-JP003356.	CC
XX	This sequence represents a truncated human delta-1 protein corresponding	CC	
PR	17-NOV-1995;	95JP-00299611.	CC
XX	to amino acids 1-702 of the mature protein (see AAW75492). The delta-1	CC	
PR	30-NOV-1995;	95JP-00311811.	CC
XX	protein is a ligand of the human notch protein and the protein or	CC	
PA	(ASAHI) ASAHI KASEI KOGYO KK.	CC	
XX	fragments, especially AAW75493-W75495, can be used as a drug to control	CC	
PI	Sakano S, Itoh A;	CC	
XX	vascular cells. The sequences were isolated and the truncated fragments	CC	
DR	were generated using the primers AAX16818-X16831	CC	
WPI; 1997-298110/27.	Sequence 702 AA;	XX	
XX	Query Match 57.0%; Score 527.5; DB 2; Length 702;	SQ	
PT	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
PT	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
PS	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
XX	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%; Score 527.5; DB 2; Length 702;	Db	663 -----GEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 699
XX	Best Local Similarity 64.8%; Pred. No. 1.6e-45;	Match	
XX	Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;	Matches	
XX	Claim 4; Page 61-64; 114pp; Japanese.	XX	
XX	The present sequence represents a polypeptide which suppresses	Qy	1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD
CC	proliferation and differentiation of undifferentiated human blood cells.	Db	568 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD
CC	such as neurons and blood cells. The polypeptide may be used for the prevention	XX	625
CC	and control of disorders involving undifferentiated cells, such as	Qy	61 LKGDDTAVRTSHSKRDTKCQSPGSRRRG-PRPHSGXACCGPGSGGTWGVSWNHCSV
CC	leukaemia and malignant tumours, and improvement of blood formation, e.g.	Db	626 LKGDDTAVRDAHSKRDTKCQPOGSSEEEKGTPPTLRG-----
CC	after immunosuppression	XX	662
XX	Sequence 702 AA;	Qy	120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS SKDTKYQSYYVISEEKDECYIA 175
SQ	Query Match 57.0%;		

PT proliferation and differentiation of undifferentiated human blood cells.
 XX
 PS Claim 15; Page 77-82; 114pp; Japanese.
 XX
 CC The present sequence represents a polypeptide which suppresses
 CC proliferation and differentiation of undifferentiated cells such as
 CC neurons and blood cells. The polypeptide may be used for the prevention
 CC and control of disorders involving undifferentiated cells, such as
 CC leukaemia and malignant tumours, and improvement of blood formation, e.g.
 CC after immunosuppression
 XX Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 2; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
 Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 2; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 684 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

RESULT 7

Qy 61 LKGDDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSSGGTWCVSSWNHCSV 119
 Db 647 LKGDDTAVRTDAHSKRDTKQPGQGSSEEKGTPPTLRG----- 683
 Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSVYVISEEKDECVIA 175
 Db 684 -----GEASERKRPDSGCSTS KDTKYQSVYVISEEKDECVIA 720

RESULT 6

Qy 61 LKGDDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSSGGTWCVSSWNHCSV 119
 Db 647 LKGDDTAVRTDAHSKRDTKQPGQGSSEEKGTPPTLRG----- 683
 Qy 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSVYVISEEKDECVIA 175
 Db 684 -----GEASERKRPDSGCSTS KDTKYQSVYVISEEKDECVIA 720

RESULT 6
 AAW75492
 ID AAW75492 standard; protein; 723 AA.
 XX
 AC AAW75492;
 XX DT 27-APR-1999 (first entry)
 XX DE Human delta-1 protein.
 XX KW Human; delta-1 protein; ligand; notch; drug; vascular cell; primer; PCR;
 KW amplification.
 XX OS Homo sapiens.
 XX FH Key
 FT Peptide 1. .21
 FT /note= "signal peptide"
 FT Protein 22. .723
 FT /note= "mature delta-1 protein"
 XX PN JP10316582-A.
 XX PD 02-DEC-1998.
 XX PP 14-MAY-1997; 97JP-00124062.
 XX PR 14-MAY-1997; 97JP-00124062.
 XX PA (ASAHI) ASAHI KASEI KOGYO KK.
 XX DR WPI; 1999-076401/07.
 DR N-PSDB; AAX16817.

XX PT Vascular cell controlling agent comprises polypeptide - which is human
 PT notch ligand and is used as drug.
 XX Disclosure; Page 16-19; 21pp; Japanese.
 XX This sequence represents the human delta-1 protein, which is a ligand of
 CC the human notch protein. The protein or fragments, especially AAW75493-
 CC W75495, can be used as a drug to control vascular cells. The sequences
 CC were isolated and the truncated fragments were generated using the

CC primers AAX16818-X16831
 CC SQ Sequence 723 AA;
 CC Query Match 57.0%; Score 527.5; DB 2; Length 723;
 CC Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 CC Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
 CC Qy 1 TMNNLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 CC 589 TMNNLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 CC SQ Sequence 723 AA;
 CC Query Match 61.0%; Score 527.5; DB 2; Length 723;
 CC Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 CC Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
 CC Qy 61 LKGDDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGSSGGTWCVSSWNHCSV 119
 CC 647 LKGDDTAVRTDAHSKRDTKQPGQGSSEEKGTPPTLRG----- 683
 CC Db 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTS KDTKYQSVYVISEEKDECVIA 175
 CC 684 -----GEASERKRPDSGCSTS KDTKYQSVYVISEEKDECVIA 720
 CC
 CC RESULT 7
 CC AAW94498
 CC ID AAW94498 standard; protein; 723 AA.
 CC XX
 CC AC AAW94498;
 CC XX DT 22-APR-1999 (first entry)
 CC XX DE Human delta-1 protein.
 CC XX KW Human; delta-1; delta-2; differentiation inhibitor; proliferation;
 CC KW leukaemia; malignant tumour.
 CC XX OS Homo sapiens.
 CC XX FH Key
 CC FT Peptide 1. .21
 CC FT /label= signal
 CC FT Protein 22. .723
 CC FT /label= Delta-1
 CC XX PN WO9851799-A1.
 CC XX PD 19-NOV-1998.
 CC XX PR 13-MAY-1998; 98WO-JP002104.
 CC XX PR 14-MAY-1997; 97JP-00124064.
 CC XX PA (ASAHI) ASAHI KASEI KOGYO KK.
 CC XX PI Sakano S;
 CC XX WPI; 1999-070120/06.
 CC DR N-PSDB; AAX16300.
 CC XX PT Peptide inhibiting the differentiation of undifferentiated blood - used
 CC PT for treatment of cancer and other disorders and the culture of human
 CC cells in vitro.
 CC XX PS Example 1; Page 64-69; 86pp; Japanese.
 CC XX WPI; 1999-070120/06.
 CC DR N-PSDB; AAX16300.
 CC
 CC The present invention describes full length and shortened human delta-2
 CC proteins. Human delta-2 is a differentiation inhibitor which inhibits the
 CC differentiation of undifferentiated cells (other than brain or muscle
 CC cells), such as blood cells, and enhances the proliferation of
 CC undifferentiated blood cells. Products of human delta-2 may be used for
 CC the treatment of diseases such as leukaemia and malignant tumours. They
 CC may also be used in the culture of human cells in vitro, e.g. for
 CC production of supplies of undifferentiated blood cells. The present
 CC sequence represents human delta-1, from an example of the present
 CC invention

XX SQ Sequence 723 AA;

Query Match 57.0*; Score 527.5; DB 2; Length 723;
Best Local Similarity 64.8*; Pred. No. 1.6e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

QY 1 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXKGDXSSDINGFQKARYPSVDYNLVQD 60
589 TMNNLANCQREKDISVSIIGATGIXNTNKKADFXKGDXSSDINGFQKARYPSVDYNLVQD 646

Db 61 LKGDDTAVRTSHSKRDTKQCSPGSRRRG-PRPHSGXACCGPGGGTGWGVSSWNHCSV 119
647 LKGDDTAVRTSHSKRDTKQCSPGSRRRG-PRPHSGXACCGPGGGTGWGVSSWNHCSV 119

QY 120 SLPKCSHAFIVDFLYFPFSGEASERKRPDSGCSTSKDTRIQSVVYISEEKDECYIA 175
Db 684 -----GEASERKRPDSGCSTSKDTRIQSVVYISEEKDECYIA 720 -----683

RESULT 8
ID AAY83227 standard; protein; 723 AA.

XX AAY83227;
XX DT 16-AUG-2000 (first entry)
DE PRO172 Polypeptide.
XX Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;
uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;
leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.
XX Homo sapiens.

OS FH Key Location/Qualifiers
Peptide 1..21 /label= signal_peptide
FT Modified-site 2..8
FT Modified-site /note= "N-myristoylation site"
FT Modified-site 37..43 /note= "N-myristoylation site"
FT Modified-site 40..46 /note= "N-myristoylation site"
FT Modified-site 93..97 /note= "Casein kinase II phosphorylation site"
FT Modified-site 98..104 /note= "Casein kinase II phosphorylation site"
FT Modified-site 99..105 /note= "N-myristoylation site"
FT Modified-site 131..135 /note= "Casein kinase II phosphorylation site"
FT Modified-site 154..158 /note= "Casein kinase II phosphorylation site"
FT Modified-site 176..185 /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 203..207 /note= "Casein kinase II phosphorylation site"
Domain 243..255 /label= EGF-like_domain
FT Modified-site 252..261 /note= "Tyrosine kinase phosphorylation site"
FT Domain 262..268 /note= "N-myristoylation site"
FT Domain 274..286 /note= "EGF-like domain"
FT Modified-site 281..287 /note= "N-myristoylation site"
FT Modified-site 282..288 /note= "N-myristoylation site"
FT Modified-site 301..307 /note= "N-myristoylation site"

XX PT Modified-site 310..316 /note= "N-myristoylation site"
Domain 314..326 /label= EGF-like_domain
FT Modified-site 328..334 /note= "N-myristoylation domain"
FT Modified-site 340..346 /note= "N-myristoylation site"
FT Modified-site 342..346 /note= "Casein kinase II phosphorylation site"
FT Modified-site 343..355 /note= "Asn and Asp hydroxylation site"
FT Modified-site 344..348 /note= "Casein kinase II phosphorylation site"
Domain 352..364 /label= EGF-like_domain
FT Modified-site 369..373 /note= "Casein kinase II phosphorylation site"
FT Modified-site 378..384 /note= "N-myristoylation site"
Domain 391..403 /label= EGF-like_domain
FT Modified-site 420..432 /note= "Asn and Asp hydroxylation site"
Domain 429..441 /label= EGF-like_domain
FT Modified-site 457..461 /note= "Casein kinase II phosphorylation site"
Domain 458..480 /note= "Asn and Asp hydroxylation site"
Domain 467..479 /label= EGF-like_domain
FT Modified-site 477..481 /note= "N-glycosylation site"
Domain 483..487 /note= "Casein kinase II phosphorylation site"
FT Modified-site 495..499 /note= "Casein kinase II phosphorylation site"
Domain 505..517 /label= EGF-like_domain
FT Modified-site 512..518 /note= "N-myristoylation site"
Domain 548..568 /label= Transmembrane_domain
FT Binding-site 552..563 /label= Prokaryotic membrane lipoprotein lipid attachment site
FT Modified-site 569..563 /note= "Casein kinase II phosphorylation site"
FT Modified-site 600..664 /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT Modified-site 670..674 /note= "Casein kinase II phosphorylation site"
FT Modified-site 671..675 /note= "Casein kinase II phosphorylation site"
FT Modified-site 676..682 /note= "N-myristoylation site"
FT Modified-site 683..689 /note= "N-myristoylation site"
FT Modified-site 695..701 /note= "N-myristoylation site"
FT Modified-site 698..702 /note= "Casein kinase II phosphorylation site"
XX PN WO200021996-A2.
XX PD 20-APR-2000.
XX PF 05-OCT-1999; 99WO-US023089.

PR 13-OCT-1998; 98US-0104080P.
 XX (GETH) GENENTECH INC.
 XX PI Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI;
 PI Yuan J;
 XX DR WPI; 2000-317943/27.
 DR N-PSDB; AAZ93703.
 XX PT Composition for inhibiting neoplastic cell growth and treating cancers of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist.
 XX PS Claim 12; Fig 8; 122pp; English.
 XX CC Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia
 XX SQ Sequence 723 AA;

Query	Match	Score	Length	DB	3;	DB	3;	Length		
	Best Local Similarity	64.8%	45;	Pred.	No.	1.6e-45;	Mismatches	723;		
	Matches	114;	Conservative	4;			Indels	45;	Gaps	4;
Qy	1	TWNNLANCOREKDISVSIIGATGIXNTNKADPXXGDXSSDKNGFQKARYPSVDYNLVQD	60							
Db	589	TWNNLANCOREKDISVSIIGATQIKNTNKADP-HGDHSADKNGF-KARYPAVDYNLVQD	646							
Qy	61	LKGDDTAVRTSHSKRDTKQCSPGSSGRRG-PRPHSGXACCGPGGGTWGVSSWNHCSV	119							
Db	647	LKGDDTAVRDAHSKRDTKQCQPQGSSEEKGTPTLRG-----	-----							
Qy	120	SLPKCNSHAFIVDFLYFPFSGEASERKRPDSGCSTSKEVKYQSVVISEEKDECVIA	175							
Db	684	-----GEASERKRPDSGCSTSKEVKYQSVVISEEKDECVIA	720							

RESULT 9
 AAB33422
 ID AAB33422 standard; protein; 723 AA.
 XX AC AAB33422;
 XX DT 29-JAN-2001 (first entry)

DE Human PRO172 protein UNQ146 SEQ ID NO:41.
 XX Human; immune related disease; diagnosis; antinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; KW antithyroid; antidiabetic; antiarthritic; antiallergic; KW haemostatic; hepatotropic; virucide; antipsoriatic; neuroprotective; KW antiaenaemic; hepatotoxic; spondyloarthropathy; systemic sclerosis; sarcoidosis; KW osteoarthritis; spondyloarthritis; systemic lupus erythematosus; rheumatoid arthritis; KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; KW autoimmune thrombocytopenia; immune-mediated renal disease; KW demyelinating disease; hepatobiliary disease; Whipple's disease; KW inflammatory bowel disease; gluten-sensitive enteropathy; KW autoimmune disease; immune-mediated skin disease; allergic disease; KW immunological disease; transplantation associated disease; KW graft rejection; graft-versus-host-disease.
 XX OS Homo sapiens.
 XX PN WO200053758-A2.
 XX PD 14-SEP-2000.
 XX PF 02-MAR-2000; 2000WO-US005841.

XX PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 12-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99WO-US008615.
 PR 28-APR-1999; 99US-0131445P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 01-SEP-1999; 99WO-US020594.
 PR 08-SEP-1999; 99WO-US028301.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX PA (GETH) GENENTECH INC.

XX XX PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W; Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V; Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX XX DR WPI; 2000-572271/53.
 XX DR N-PSDB; AAC58587.

XX PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 XX XX PA Claim 33; Fig 18; 309pp; English.

XX CC The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, immune-mediated renal disease; KW demyelinating disease; hepatobiliary disease; Whipple's disease; KW inflammatory bowel disease; gluten-sensitive enteropathy; KW autoimmune disease; immune-mediated skin disease; allergic disease; KW immunological disease; transplantation associated disease; KW graft rejection; graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477

CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention
 XX

SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
 XX

Qy 1 TMNQLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFOKARYPSVDYNLVQD 60
 Db 589 TMNQLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 XX

Qy 61 LKGDDTAVRTSHSKRDTKQCSPGSSGRRRG-PRPHSGXACCGPGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQCQGSSGEKGTPTTLRG----- 683
 XX

Qy 120 SLPKCASHAFIVDFLYPPFSGEASERKRPDSCGCSTSCKTQSVVVISSEEKDECVIA 175
 Db 684 -----GEASERKRPDSCGCSTSCKTQSVVVISSEEKDECVIA 720
 XX

RESULT 10

AAB24388

ID AAB24388 standard; protein; 723 AA.

XX

AC AAB24388;

XX

DT 07-NOV-2000 (first entry)

XX

DE Human PRO172 protein sequence SEQ ID NO:4.

XX

KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
 cytostatic; gene therapy; vaccine.
 XX

OS Homo sapiens.
 XX

PN WO2000032221-A2.

XX

PD 08-JUN-2000.

XX

PF 30-NOV-1999; 99WO-US028313.

XX

PR 01-DEC-1998; 98WO-US025108.

PR 16-DEC-1998; 98US-0112850P.

PR 12-JAN-1999; 99US-0115554P.

PR 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-0134287P.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-OCT-1999; 99US-0162506P.

XX

(GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillian KJ,
 Goddard A, Godowski PJ, Gurney AL, Klein RD,
 Smith V, Watanabe CK, Williams PM, Wood WI;
 XX

DR WPI; 2000-412154/35.
 DR N-PSDB; AAA77512.

Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 PT and treating disorders a cardiovascular, endothelial or angiogenic
 PT disorders in mammals.
 XX

SQ Claim 72; Fig 2; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders a
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the prevention,
 CC treatment and diagnosis of diseases associated with inappropriate PRO
 CC expression such as cardiovascular, endothelial or angiogenic disorders in
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
 CC example, the nucleic acids (NCS) and vectors containing them and the PRO
 CC polypeptide may be used to treat disorders associated with decreased PRO
 CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
 CC nucleotide and protein sequences used in the exemplification of the
 CC present invention
 XX

SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
 XX

Qy 1 TMNQLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFOKARYPSVDYNLVQD 60
 Db 589 TMNQLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 XX

Qy 61 LKGDDTAVRTSHSKRDTKQCSPGSSGRRRG-PRPHSGXACCGPGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQCQGSSGEKGTPTTLRG----- 683
 XX

Qy 120 SLPKCASHAFIVDFLYPPFSGEASERKRPDSCGCSTSCKTQSVVVISSEEKDECVIA 175
 Db 684 -----GEASERKRPDSCGCSTSCKTQSVVVISSEEKDECVIA 720
 XX

SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 3; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
 XX

Qy 1 TMNQLANCOREKDISVSIIGATGIXNTNKKADFXGDXSSDKNGFOKARYPSVDYNLVQD 60
 Db 589 TMNQLANCOREKDISVSIIGATQIKNTNKKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 XX

Qy 61 LKGDDTAVRTSHSKRDTKQCSPGSSGRRRG-PRPHSGXACCGPGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQCQGSSGEKGTPTTLRG----- 683
 XX

Qy 120 SLPKCASHAFIVDFLYPPFSGEASERKRPDSCGCSTSCKTQSVVVISSEEKDECVIA 175
 Db 684 -----GEASERKRPDSCGCSTSCKTQSVVVISSEEKDECVIA 720
 XX

RESULT 11
 AAY79032 standard; protein; 723 AA.
 ID AAY79032 (first entry)
 XX

AC AAY79032;
 XX

DT 06-JUN-2000 (first entry)
 XX

DE Human delta protein amino acid sequence.
 XX

AC AAY79032;
 XX

DT 06-JUN-2000 (first entry)
 XX

DE Human delta protein amino acid sequence.
 XX

Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;
 lung; melanoma; seminoma; central nervous system disorder; psoriasis;
 tissue regeneration; liver cirrhosis; keloid formation; baldness;
 inner ear disorder; human.
 XX

Homo sapiens.
 XX

WO200002897-A2.
 XX

PN WO200002897-A2.
 XX

PR 20-JAN-2000.
 XX

PR 13-JUL-1999; 99US-0141037P.
 PR 26-JUL-1999; 99US-0144758P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 XX

PR 13-JUL-1999; 99US-0092513P.
 PR 19-OCT-1999; 99US-0104834P.
 XX

(UYA) UNIV YALE.
 XX

PR Artavanis-Tsakonas S, Rand MD, Q1 H;
 XX

PR WPI; 2000-282852/24.
 DR N-PSDB; AAZ98679.
 XX

FT Domain 467. .479
 FT /label= "EGF-like domain cysteine pattern signature"
 FT Modified-site 477. .481
 FT /note= "N-glycosylation site"
 FT Modified-site 483. .487
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 495. .499
 FT /note= "Casein kinase II phosphorylation site"
 FT Domain 505. .517
 FT /label= "EGF-like domain cysteine pattern signature"
 FT Modified-site 512. .518
 FT /note= "N-myristoylation site"
 FT Binding-site 548. .568
 FT /label= "Transmembrane domain"
 FT Modified-site 552. .563
 FT /label= "Prokaryotic membrane lipoprotein lipid a"
 FT Modified-site 659. .663
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 660. .664
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 670. .674
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 671. .675
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 676. .682
 FT /note= "N-myristoylation site"
 FT Modified-site 683. .689
 FT /note= "N-myristoylation site"
 FT Modified-site 695. .701
 FT /note= "N-myristoylation site"
 FT Modified-site 698. .702
 FT /note= "Casein kinase II phosphorylation site"
 PN WO200055319-A1.
 XX 21-SEP-2000.
 XX 02-DEC-1999; 99WO-US028564.
 XX (GETH) GENENTECH INC.
 XX DR; N-PSDB; AAA54105.
 XX WPI; 2000-638201/61.
 PI Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
 PI Yuan J;
 XX PT PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukemia and for identifying compounds capable of inhibiting growth of neoplastic cells.
 XX PS Claim 31; Fig 8; 133pp; English.
 XX Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their agonists (preferably anti-PRO agonist antibody or a small molecule mimicking the biological activity of PRO polypeptide) are useful in vitro or in vivo for inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic cell growth and for treating cancer including breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, central nervous system cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, glial, astrocytal,

CC hypothalamic and other glandular, macrophagal, epithelial, stromal, CC blastocoelic disorders and inflammatory, angiogenic and immunologic CC disorders as well as being useful for identifying agonists to PRO CC polypeptides by contacting the polypeptide with a candidate molecule and CC monitoring biological activity mediated by the polypeptide
 CC Sequence 723 AA;
 SQ Query Match 57.0%; Score 527.5; DB 3; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCOREKDISVSIIGATGXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCOREKDISVSIIGATQIKNTNKCADF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 Qy 61 LKGDDTAVRTSHSKRDTKQCSPGSGRRRG-PRPHSGXACCGPGSGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQPOGSGBEKGTPRTLRG----- 683
 Qy 120 SLPKCSHAFTIVDFLYPPFGEASERKRPDGCSTSCKDTKYQSYYVISEEKDECIVIA 175
 Db 684 -----GEASERKRPDGCSTSCKDTKYQSYYVISEEKDECIVIA 720

RESULT 13
 ARU12344 ID AAU12344 standard; protein; 723 AA.
 XX AAU12344;
 AC XX DT 24-OCT-2001 (first entry)
 DE XX Human PRO172 polypeptide sequence.
 KW XX Human secretary and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIA; gene therapy.
 OS XX Homo sapiens.
 PN WO200140466-A2.
 XX PD 07-JUN-2001.
 PF XX 01-DEC-2000; 2000WO-US032678.
 XX PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Beressini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX DR; WPI: 2001-408281/43.
 XX PT Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT Other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX PS Claim 12; Fig 346; 813pp; English.
 XX CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX SQ Sequence 723 AA;

Query Match 57.0%; Score 527.5; DB 4; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

Qy 1 TMNNLANCQREKDISVIIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
 Db 589 TMNNLANCQREKDISVIIIGATQIKNTNKADP-HGDHSADKNGP-KARYPAVDYNLVQD 646

Qy 61 LKGDDTAVRTSHSKRDTKQSPGSSGRRRG-PRPHSGXACCGPGGGGTWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQPGSSGEEKGPTTLRG----- - 683

Qy 120 SI.PPKCSHAFIVDFLYPPFSGEASERKRPDSGCSTSKDTRKYQSYYVISEEKDECVIA 175
 Db 684 ----- -GEASERKRPDSGCSTSKDTRKYQSYYVISEEKDECVIA 720

RESULT 14
 AAB53064

ID AAB53064 standard; protein; 723 AA.
 XX AAB53064;
 AC XX DT 28-FEB-2001 (first entry)
 DE XX Human angiogenesis-associated protein PRO172, SEQ ID NO:2.
 XX KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX OS Homo sapiens.
 XX PN WO200053753-A2.
 XX PD 14-SEP-2000.
 XX PF 05-JAN-2000; 2000WO-US000219.
 XX PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.

XX (GETH) GENENTECH INC.
 XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX DR; WPI: 2001-090793/10.
 XX DR N-PSDB; AAC97368.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic
 PT disorders, such as atherosclerosis, wounds or cancer.
 XX PA (GETH) GENENTECH INC.
 XX PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX DR; WPI: 2001-090793/10.
 XX DR N-PSDB; AAC97368.

XX Claim 69; Fig 2; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO

nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the invention

nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the invention

Sequence 723 AA;

Query Match 57. 0%; Score 527. 5; DB 4; Length 723;
Best Local Similarity 64. 8%; Pred. NO. 1. 6e-45;
Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;

1 TMNNLANCOREKDISVSIIGATGIXNTNKADFXGDXSSDKNGFQKARYPSVDYNLVQD 60
589 TMNNLANCQREKDISVSIIGATQIKNTNKADF-HGDHSADKNGF-KARYPAVDYNLVQD 646

61 LKGDDTAVRTSHSKRDTKQCQSPGSSGRRG-PRPHSGXACCGPGSGGGTWGVSSWNHCSV 119
647 LKGDDTAVRDAHSKRDTCQPKQGSSGEEKGTPTTLRG----- 683

120 SLPKCSHAIFIYDFLYFPFSGEASERKRPDSGCSTSKDTRKYQSYYVISEEKDECVIA 175
684 ----- 683

RESULT 15
ABO17788 standard; protein; 723 AA.
ABO17788;
26-AUG-2003 (first entry)

Novel human secreted and transmembrane protein PRO172.
Human; secreted and transmembrane protein; PRO; antiinflammatory; antiatherosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing.

Homo sapiens.
US2003032156-A1.
13-FEB-2003.

06-MAY-2002; 2002US-00140474.

PR 14-SEP-1998; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.

Search completed: December 2, 2004, 03:58:02
 Job time : 156 secs

PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX DR WPI; 2003-341980/32.
 XX DR N-PSDB; ACD24025.
 PT New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.
 XX PS Claim 12; Fig 346; 660pp; English.
 XX CC The invention describes an isolated nucleic acid (I) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (I) is used to
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
 CC the proliferation or differentiation of cells or gene expression,
 CC stimulate the release of proteoglycans, stimulate the release of cytokine
 CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
 CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
 CC acid and polypeptide encoded by it, are useful for treating inflammatory
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, acquired immunodeficiency syndrome
 CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
 CC hybridisation probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
 CC This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX SQ Sequence 723 AA:
 Query Match 57.0%; Score 527.5; DB 6; Length 723;
 Best Local Similarity 64.8%; Pred. No. 1.6e-45;
 Matches 114; Conservative 4; Mismatches 13; Indels 45; Gaps 4;
 Qy 1 TMNNLANCQREKDISVSIIGATGIXNTNKAKDFXXGDXSSDKNGFQOKARYPPSVDYNLVQD 60
 Db 589 TMNNLANCQREKDISVSIIGATQIKNTNKAKDF-HGDHSADKNGF-KARYPAVDYNLVQD 646
 Qy 61 LKGDDTAVRTSHSKRDTKQSFQSSGRRG-PRPHSGXACCGPGGGTGWGVSSWNHCSV 119
 Db 647 LKGDDTAVRDAHSKRDTCQPGSSGEEKGTPPTLRG----- 683
 Qy 120 SLPKCSHAFIVDELYFPFSGEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 175
 Db 684 -----GEASERKRPDSGCSTS KDTKYQSYYVISEEKDECVIA 720